

091830-972

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:30:21 ; Search time 1723.65 Seconds  
(without alignments)  
3963.787 Million cell updates/sec

Title: US-09-830-972-32  
Perfect score: 705  
Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094842\_18348/app\_query.fasta\_1  
.3683

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_@CGN\_1\_1\_19954\_@runat\_14042005\_094842\_18348 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
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2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

6-21-05

```

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	680.5	96.5	1568	10	RNO242963	AJ242963 Rattus no
2	635.5	90.1	1769	10	AY102283	AY102283 Mus muscu
3	589.5	83.6	764	10	AF051335	AF051335 Rattus no
4	581.5	82.5	734	10	AF326337	AF326337 Mus muscu
5	572.5	81.2	1079	9	BC007109	BC007109 Homo sapi
6	572.5	81.2	1151	9	BC001035	BC001035 Homo sapi
7	572.5	81.2	1691	9	AF132048	AF132048 Homo sapi
8	572.5	81.2	1698	9	BC014366	BC014366 Homo sapi
9	572.5	81.2	1700	9	AF177332	AF177332 Homo sapi
10	572.5	81.2	1800	9	AY102276	AY102276 Homo sapi
11	571.5	81.1	1213	6	BD194907	BD194907 86 human
12	571.5	81.1	1213	6	CQ855235	CQ855235 Sequence
13	565	80.1	1721	4	AY164744	AY164744 Bos tauru
14	563.5	79.9	2162	9	AB049853	AB049853 Macaca fa
15	559.5	79.4	2610	6	AR379837	AR379837 Sequence
16	558	79.1	1617	9	AF087901	AF087901 Homo sapi
17	531	75.3	799	6	AR028522	AR028522 Sequence
18	525	74.5	994	6	BD139293	BD139293 Extended
19	509.5	72.3	404	6	BD076183	BD076183 5' EST of
20	503	71.3	600	9	HSA251385	AJ251385 Homo sapi
21	485	68.8	1363	5	BX933922	BX933922 Gallus ga
22	485	68.8	1578	5	CR353502	CR353502 Gallus ga
23	482	68.4	1597	5	AY164737	AY164737 Gallus ga
24	470.5	66.7	639	6	AX410838	AX410838 Sequence
25	455	64.5	4822	6	AR220865	AR220865 Sequence
26	447	63.4	1738	10	AB073672	AB073672 Mus muscu
27	447	63.4	2481	9	AF063601	AF063601 Homo sapi
28	447	63.4	2883	9	AF320999	AF320999 Homo sapi
29	447	63.4	2958	10	BC032192	BC032192 Mus muscu
30	447	63.4	2974	6	CQ716296	CQ716296 Sequence
31	447	63.4	3489	6	AX766046	AX766046 Sequence
32	447	63.4	3491	9	AF333336	AF333336 Homo sapi
33	447	63.4	3492	6	CQ829507	CQ829507 Sequence
34	447	63.4	3576	6	AX766050	AX766050 Sequence
35	447	63.4	3579	6	BD249446	BD249446 Protein s
36	447	63.4	3579	9	HSA251383	AJ251383 Homo sapi
37	447	63.4	3815	10	BC032272	BC032272 Mus muscu
38	447	63.4	3919	6	CQ829486	CQ829486 Sequence
39	447	63.4	4053	6	AX195249	AX195249 Sequence
40	447	63.4	4053	9	AB020693	AB020693 Homo sapi
41	447	63.4	4060	9	AY123250	AY123250 Homo sapi
42	447	63.4	4063	10	AY102280	AY102280 Mus muscu
43	447	63.4	4070	9	AY123249	AY123249 Homo sapi

44	447	63.4	4093	6	BD270070	BD270070 Secreted
45	447	63.4	4102	9	AY123245	AY123245 Homo sapi

# ALIGNMENTS

## RESULT 1

RNO242963

LOCUS RNO242963 1568 bp mRNA linear ROD 28-JAN-2000

DEFINITION Rattus norvegicus mRNA for Nogo-C protein.

ACCESSION AJ242963

VERSION AJ242963.1 GI:6822250

KEYWORDS Nogo-C protein.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

## REFERENCE 1

AUTHORS Chen,M.S., Huber,A.B., van der Haar,M.E., Frank,M., Schnell,L.,  
Spillmann,A.A., Christ,F. and Schwab,M.E.

TITLE Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
antigen for monoclonal antibody IN-1

JOURNAL Nature 403 (6768), 434-439 (2000)

MEDLINE 20129258

PUBMED 10667796

## REFERENCE 2 (bases 1 to 1568)

AUTHORS Van der Haar,M.E.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-1999) Van der Haar M.E., Department of  
Neuromorphology, Brain Research Institute, University of Zurich,  
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND

COMMENT Related sequences: AJ242961-2.

## FEATURES

source

Location/Qualifiers

1. .1568

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

gene

1. .1568

/gene="nogo-C"

CDS

118. .717

/gene="nogo-C"

/function="unknown"

/note="The nogo gene encodes different transcripts. Nogo-A  
en -C have a unique 5' end but share the same 3' end"

/codon\_start=1

/product="Nogo-C protein"

/protein\_id="CAB71029.1"

/db\_xref="GI:6822251"

/db\_xref="GOA:Q9JK11"

/db\_xref="UniProt/Swiss-Prot:Q9JK11"

/translation="MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIV  
SVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA  
LGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSIPV  
IYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD"

## ORIGIN

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:29:46 ; Search time 199.52 Seconds  
(without alignments)  
4183.459 Million cell updates/sec

Title: US-09-830-972-32  
Perfect score: 705  
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094842\_18342/app\_query.fasta\_1  
.3683

-DB=N\_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972 @CGN\_1\_1\_1955 @runat\_14042005\_094842\_18342 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*



11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	680.5	96.5	1568	3	AAD01175	Aad01175 Rat neuri
2	581.5	82.5	734	12	ADF42781	Adf42781 Mouse CYP
3	572.5	81.2	1798	6	ABK90135	Abk90135 DNA encod
4	571.5	81.1	668	6	ABL89601	Abl89601 Human pol
5	571.5	81.1	1213	2	AAX04379	Aax04379 Human sec
6	566	80.3	1785	12	ADK14166	Adk14166 Human aut
7	559.5	79.4	2610	11	ADI31056	Adi31056 Human cDN
8	553.5	78.5	770	3	AAA72983	Aaa72983 Human NSP
9	531	75.3	431	8	ABX37040	Abx37040 Bovine ES
10	531	75.3	799	2	AAV23695	Aav23695 Human NSP
11	525	74.5	991	2	AAX97587	Aax97587 Extended
12	525	74.5	994	12	ADP18854	Adp18854 Human sec
13	509.5	72.3	404	2	AAX41193	Aax41193 Human sec
14	503	71.3	600	4	AAF90323	Aaf90323 Human NOG
15	500	70.9	389	8	ABX39989	Abx39989 Bovine ES
16	470.5	66.7	639	6	ABN96987	Abn96987 Gene #348
17	455	64.5	4822	6	ABS70449	Abs70449 Human bon
18	447	63.4	3492	12	ADP45571	Adp45571 Rat NogoA
19	447	63.4	3579	3	AAZ56886	Aaz56886 Human MAG
20	447	63.4	3579	4	AAF90324	Aaf90324 Human NOG
21	447	63.4	3579	6	ABK90134	Abk90134 DNA encod
22	447	63.4	3579	6	ABN86601	Abn86601 Human neu
23	447	63.4	3579	12	ADO07886	Ado07886 Human pol
24	447	63.4	3579	12	ADR13965	Adr13965 Human NOG
25	447	63.4	3833	3	AAD01174	Aad01174 Bovine ne
26	447	63.4	3919	12	ADP45550	Adp45550 Human Nog
27	447	63.4	4053	4	AAS09453	Aas09453 Human cDN
28	447	63.4	4053	9	ACC81048	Acc81048 Human Nog
29	447	63.4	4053	12	ADP13574	Adp13574 Renal cel
30	447	63.4	4093	3	AAA23454	Aaa23454 cDNA enco
31	447	63.4	4632	6	ABV94680	Abv94680 Human pan
32	447	63.4	4632	10	ADG32772	Adg32772 Human DNA
33	447	63.4	4684	3	AAD01173	Aad01173 Rat neuri
34	447	63.4	4684	6	ABN86600	Abn86600 Rat neuro
35	447	63.4	4698	8	ABX34563	Abx34563 Human mdd
36	447	63.4	4789	13	ADR83534	Adr83534 Human ret
37	443	62.8	1122	3	AAZ56888	Aaz56888 Human MAG
38	443	62.8	1122	4	AAF90325	Aaf90325 Human NOG
39	443	62.8	1216	6	ABA05903	Aba05903 Human RTN
40	443	62.8	1599	10	ADI62860	Adi62860 Human apo
41	443	62.8	1610	3	AAZ36230	Aaz36230 cDNA enco
42	443	62.8	1683	4	AAD08386	Aad08386 Human sec
c 43	443	62.8	1758	4	AAF32725	Aaf32725 Human sec
44	443	62.8	2052	6	ABK90133	Abk90133 DNA encod

## ALIGNMENTS

## RESULT 1

AAD01175

ID AAD01175 standard; cDNA; 1568 BP.

XX

AC AAD01175;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo C cDNA.

XX

KW Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS

1. .1566

FT /\*tag= a

FT /product= "Nogo C protein (residues 40-238) flanked by 1-  
 FT 39 residues at the N-terminal and 239-522 residues at the  
 FT C-terminal"

FT /transl\_except= (pos:7. .9, aa:Xaa)

FT /transl\_except= (pos:85. .87, aa:Xaa)

FT /transl\_except= (pos:787. .789, aa:Xaa)

FT /transl\_except= (pos:826. .828, aa:Xaa)

FT /transl\_except= (pos:841. .843, aa:Xaa)

FT /transl\_except= (pos:883. .885, aa:Xaa)

FT /transl\_except= (pos:889. .891, aa:Xaa)

FT /transl\_except= (pos:940. .942, aa:Xaa)

FT /transl\_except= (pos:952. .954, aa:Xaa)

FT /transl\_except= (pos:1003. .1005, aa:Xaa)

FT /transl\_except= (pos:1111. .1113, aa:Xaa)

FT /transl\_except= (pos:1120. .1122, aa:Xaa)

FT /transl\_except= (pos:1138. .1140, aa:Xaa)

FT /transl\_except= (pos:1216. .1218, aa:Xaa)

FT /transl\_except= (pos:1222. .1224, aa:Xaa)

FT /transl\_except= (pos:1228. .1230, aa:Xaa)

FT /transl\_except= (pos:1264. .1266, aa:Xaa)

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FT /transl\_except= (pos:1357. .1359, aa:Xaa)

FT /transl\_except= (pos:1393. .1395, aa:Xaa)

FT /transl\_except= (pos:1444. .1446, aa:Xaa)

FT /transl\_except= (pos:1537. .1539, aa:Xaa)

FT /note= "Xaa corresponds to in-frame stop codon; the CDS  
 FT does not end in a stop codon"

FT /partial

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:35:57 ; Search time 61.5766 Seconds  
(without alignments)  
3746.799 Million cell updates/sec

Title: US-09-830-972-32  
Perfect score: 705  
Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094844\_18372/app\_query.fasta\_1  
.3683

-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_@CGN\_1\_1\_255\_@runat\_14042005\_094844\_18372 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

		8					
Result	No.	Score	Query		DB	ID	Description
			Match	Length			
	1	572.5	81.2	1669	4	US-09-949-016-3253	Sequence 3253, Ap
	2	559.5	79.4	2610	4	US-09-023-655-382	Sequence 382, App
	3	531	75.3	799	2	US-08-700-607-2	Sequence 2, Appli
	4	455	64.5	4822	3	US-09-484-970B-106	Sequence 106, App
	5	337	47.8	2069	4	US-09-949-016-3309	Sequence 3309, Ap
	6	337	47.8	3202	4	US-09-949-016-1127	Sequence 1127, Ap
c	7	335	47.5	601	4	US-09-949-016-117588	Sequence 117588,
c	8	335	47.5	601	4	US-09-949-016-117589	Sequence 117589,
	9	335	47.5	42075	4	US-09-949-016-14995	Sequence 14995, A
	10	311	44.1	3517	4	US-09-799-451-111	Sequence 111, App
	11	309	43.8	1766	3	US-09-149-476-254	Sequence 254, App
	12	309	43.8	2262	4	US-09-949-016-2988	Sequence 2988, Ap
	13	309	43.8	2664	3	US-09-149-476-255	Sequence 255, App
	14	305	43.3	1095	2	US-08-700-607-4	Sequence 4, Appli
	15	297	42.1	443	4	US-09-513-999C-3784	Sequence 3784, Ap
	16	270	38.3	261	2	US-08-700-607-9	Sequence 9, Appli
c	17	268	38.0	601	4	US-09-949-016-40169	Sequence 40169, A
c	18	268	38.0	601	4	US-09-949-016-119335	Sequence 119335,
	19	268	38.0	135667	4	US-09-949-016-15051	Sequence 15051, A
	20	268	38.0	152486	4	US-09-949-016-12869	Sequence 12869, A
	21	261	37.0	13906	4	US-09-949-016-14730	Sequence 14730, A
	22	250	35.5	2014	4	US-09-270-767-13561	Sequence 13561, A
	23	229.5	32.6	794	3	US-09-149-476-102	Sequence 102, App
	24	214	30.4	2181	4	US-09-949-016-1419	Sequence 1419, Ap
	25	177	25.1	15661	4	US-09-949-016-13161	Sequence 13161, A
c	26	129	18.3	601	4	US-09-949-016-117566	Sequence 117566,
c	27	101	14.3	601	4	US-09-949-016-48087	Sequence 48087, A
	28	99	14.0	425	3	US-08-905-223-178	Sequence 178, App
c	29	86	12.2	3042	4	US-09-762-724-1	Sequence 1, Appli
	30	79.5	11.3	80355	4	US-09-949-016-12735	Sequence 12735, A
	31	79.5	11.3	80357	4	US-09-949-016-13572	Sequence 13572, A
	32	78	11.1	2535	3	US-09-422-936-46	Sequence 46, Appl
	33	78	11.1	2883	3	US-09-422-936-44	Sequence 44, Appl
	34	76.5	10.9	1797	2	US-08-853-659A-28	Sequence 28, Appl
	35	76.5	10.9	8967	2	US-08-853-659A-6	Sequence 6, Appli
c	36	76.5	10.9	8967	2	US-08-853-659A-9	Sequence 9, Appli
	37	76.5	10.9	8967	2	US-08-853-659A-64	Sequence 64, Appl
c	38	76.5	10.9	8967	2	US-08-853-659A-67	Sequence 67, Appl
	39	76.5	10.9	24701	2	US-08-853-659A-2	Sequence 2, Appli
c	40	76.5	10.9	24701	2	US-08-853-659A-3	Sequence 3, Appli
	41	76.5	10.9	24701	2	US-08-853-659A-60	Sequence 60, Appl
c	42	76.5	10.9	24701	2	US-08-853-659A-61	Sequence 61, Appl
c	43	76.5	10.9	40429	4	US-08-311-731A-125	Sequence 125, App
c	44	75.5	10.7	897	4	US-09-248-796A-3257	Sequence 3257, Ap
c	45	75	10.6	1426	3	US-09-121-425-4	Sequence 4, Appli

## ALIGNMENTS

RESULT 1

US-09-949-016-3253

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 22:42:49 ; Search time 216.627 Seconds  
(without alignments)  
3948.747 Million cell updates/sec

Title: US-09-830-972-32  
Perfect score: 705  
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Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: \ 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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.3683

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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query		DB	ID	Description
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1	572.5	81.2	1160	14	US-10-175-523-156	Sequence 156, App
2	572.5	81.2	1798	18	US-10-466-258-10	Sequence 10, Appl
3	571.5	81.1	668	17	US-10-264-237-163	Sequence 163, App
4	566	80.3	1785	17	US-10-439-388-62	Sequence 62, Appl
5	559.5	79.4	2610	17	US-10-641-643-382	Sequence 382, App
6	531	75.3	431	9	US-09-960-352-2205	Sequence 2205, Ap
7	531	75.3	799	17	US-10-660-946-2	Sequence 2, Appli
8	525	74.5	994	11	US-09-978-360A-110	Sequence 110, App
9	500	70.9	389	9	US-09-960-352-5154	Sequence 5154, Ap
10	470.5	66.7	639	9	US-09-880-107-3484	Sequence 3484, Ap
11	447	63.4	3579	9	US-09-789-386-1	Sequence 1, Appli
12	447	63.4	3579	9	US-09-893-348-22	Sequence 22, Appl
13	447	63.4	3579	17	US-10-267-502-212	Sequence 212, App
14	447	63.4	3579	18	US-10-327-213-8	Sequence 8, Appli
15	447	63.4	3579	18	US-10-466-258-8	Sequence 8, Appli
16	447	63.4	3579	18	US-10-810-653-22	Sequence 22, Appl
17	447	63.4	4053	9	US-09-758-140-5	Sequence 5, Appli
18	447	63.4	4053	9	US-09-972-599A-5	Sequence 5, Appli
19	447	63.4	4053	18	US-10-717-597-310	Sequence 310, App
20	447	63.4	4632	14	US-10-060-036-53	Sequence 53, Appl
21	447	63.4	4684	9	US-09-893-348-17	Sequence 17, Appl
22	447	63.4	4684	18	US-10-810-653-17	Sequence 17, Appl
23	443	62.8	1122	9	US-09-789-386-5	Sequence 5, Appli
24	443	62.8	1610	9	US-09-765-205-5	Sequence 5, Appli
25	443	62.8	2052	18	US-10-466-258-3	Sequence 3, Appli
26	443	62.8	2235	14	US-10-060-036-54	Sequence 54, Appl
27	443	62.8	2782	15	US-10-205-194-165	Sequence 165, App
28	441	62.6	1980	17	US-10-220-891-22	Sequence 22, Appl
29	436.5	61.9	3492	17	US-10-267-502-214	Sequence 214, App
30	383	54.3	1514	9	US-09-823-245A-349	Sequence 349, App
31	349	49.5	1473	15	US-10-205-194-128	Sequence 128, App
32	349	49.5	1502	15	US-10-205-219-94	Sequence 94, Appl
33	349	49.5	1520	15	US-10-084-817-333	Sequence 333, App
34	340	48.2	422	9	US-09-960-352-11567	Sequence 11567, A
35	337	47.8	2331	17	US-10-267-502-213	Sequence 213, App

36	337	47.8	2343	17	US-10-267-502-215	Sequence 215, App
37	337	47.8	3202	9	US-09-954-456-210	Sequence 210, App
38	337	47.8	3202	17	US-10-172-118-386	Sequence 386, App
39	337	47.8	3202	17	US-10-342-887-386	Sequence 386, App
40	337	47.8	3202	18	US-10-723-860-1480	Sequence 1480, Ap
41	337	47.8	3202	19	US-10-843-641A-3237	Sequence 3237, Ap
42	337	47.8	3305	18	US-10-723-860-5926	Sequence 5926, Ap
43	335	47.5	60615	18	US-10-633-423-9	Sequence 9, Appli
44	335	47.5	60615	18	US-10-427-741-9	Sequence 9, Appli
45	311	44.1	3517	17	US-10-302-172-111	Sequence 111, App

#### ALIGNMENTS

##### RESULT 1

US-10-175-523-156

; Sequence 156, Application US/10175523

; Publication No. US20030096264A1

; GENERAL INFORMATION:

; APPLICANT: Brockman, Jeffrey

; APPLICANT: Evans, David

; APPLICANT: Hook, Derek

; APPLICANT: Klimczak, Leszek

; APPLICANT: Laeng, Pascal

; APPLICANT: Palfreyman, Michael

; APPLICANT: Rajan, Prithi

; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)

; FILE REFERENCE: 3235/1J795-US3

; CURRENT APPLICATION NUMBER: US/10/175,523

; CURRENT FILING DATE: 2002-06-18

; PRIOR APPLICATION NUMBER: US 60/299,151

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/317,828

; PRIOR FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: US 60/325,150

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US 60/333,047

; PRIOR FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: US 60/349,936

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US 60/361,834

; PRIOR FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 197

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 156

; LENGTH: 1160

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-175-523-156

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Pred. No.:	2.07e-68	Length:	1160
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Percent Similarity:	90.00%	Conservative:	3
Best Local Similarity:	87.86%	Mismatches:	11
Query Match:	81.21%	Indels:	3
DB:	14	Gaps:	1

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:34:27 ; Search time 1246.52 Seconds  
(without alignments)  
4305.640 Million cell updates/sec

Title: US-09-830-972-32  
Perfect score: 705  
Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	644.5	91.4	791	7	CF977898	CF977898 F26A06_04
4	635.5	90.1	718	1	AA986233	AA986233 uc73g12.y
5	635.5	90.1	813	5	BU848611	BU848611 AGENCOURT
6	635.5	90.1	921	5	BU503291	BU503291 AGENCOURT
7	627.5	89.0	595	7	CK617525	CK617525 mk06d10.y
8	627.5	89.0	826	7	CK791443	CK791443 AGENCOURT
9	622.5	88.3	424	5	BY262542	BY262542 BY262542
10	618.5	87.7	749	4	BG296048	BG296048 602393712
c 11	609.5	86.5	1054	7	CR755232	CR755232 CR755232
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13	581.5	82.5	799	1	AU080133	AU080133 AU080133
14	579.5	82.2	504	2	BF671520	BF671520 602151450
15	579.5	82.2	606	2	BF670363	BF670363 602150242
16	579.5	82.2	678	2	BF672234	BF672234 602150421
17	579.5	82.2	740	4	BG698839	BG698839 602703243
18	579	82.1	1057	7	CR753971	CR753971 CR753971
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22	578	82.0	805	7	CO735185	CO735185 SILE04c10
23	576.5	81.8	876	2	BF574724	BF574724 602134511
24	575.5	81.6	747	4	BG623462	BG623462 602648520
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# ALIGNMENTS

GenCore version 5.1.6  
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Run on: April 16, 2005, 11:30:21 ; Search time 14217.1 Seconds  
(without alignments)  
3963.787 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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.3683

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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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4: gb\_om:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query						Description
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	4	5312.5	90.8	4627	10	AY102284	AY102284 Mus muscu
	5	5307	90.7	3821	10	AY114152	AY114152 Mus muscu
	6	5303.5	90.7	4518	10	BC056373	BC056373 Mus muscu
	7	4501.5	77.0	4063	10	AY102280	AY102280 Mus muscu
	8	4403.5	75.3	3919	6	CQ829486	CQ829486 Sequence
	9	4403.5	75.3	4053	6	AX195249	AX195249 Sequence
	10	4403.5	75.3	4053	9	AB020693	AB020693 Homo sapi
	11	4403.5	75.3	4166	9	AB040462	AB040462 Homo sapi
	12	4403.5	75.3	4632	9	AF148537	AF148537 Homo sapi
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	22	3931	67.2	238341	2	AC133315	AC133315 Rattus no
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	26	3720.5	63.6	3491	9	AF333336	AF333336 Homo sapi
	27	3714	63.5	4123	9	AY123247	AY123247 Homo sapi
	28	3711	63.5	4160	9	AY123246	AY123246 Homo sapi
	29	3708.5	63.4	4070	9	AY123249	AY123249 Homo sapi
	30	3700	63.3	4060	9	AY123250	AY123250 Homo sapi
	31	3584	61.3	2248	6	CQ814526	CQ814526 Sequence
	32	3575	61.1	2278	6	CQ814528	CQ814528 Sequence
	33	3495.5	59.8	60615	10	AY102286	AY102286 Mus muscu
	34	3495.5	59.8	166516	2	AC135510	AC135510 Mus muscu
	35	3495.5	59.8	211357	2	AC113284	AC113284 Mus muscu
	36	3495.5	59.8	212042	10	AL929371	AL929371 Mouse DNA
	37	3447.5	59.0	2883	9	AF320999	AF320999 Homo sapi
	38	3407.5	58.3	2974	6	CQ716296	CQ716296 Sequence
	39	3065	52.4	2958	10	BC032192	BC032192 Mus muscu
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	42	2737.5	46.8	90756	9	AY102285	AY102285 Homo sapi
c	43	2737.5	46.8	162692	2	AC016171	AC016171 Homo sapi

44 2632.5 45.0 2386 6 BD190738  
45 2632.5 45.0 2386 6 AX099401

BD190738 Secreted  
AX099401 Sequence

#### ALIGNMENTS

##### RESULT 1

AX766046

LOCUS AX766046 3489 bp DNA linear PAT 25-JUN-2003

DEFINITION Sequence 1 from Patent WO03002602.

ACCESSION AX766046

VERSION AX766046.1 GI:32260128

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1

AUTHORS Eisenbach-Schwartz, M. and Hauben, E.

TITLE Nogo and nogo receptor derived peptides for t-cell mediated  
neuroprotection

JOURNAL Patent: WO 03002602-A 1 09-JAN-2003;  
YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)

FEATURES Location/Qualifiers

source

1. .3489

/organism="Rattus norvegicus"

/mol\_type="unassigned DNA"

/db\_xref="taxon:10116"

exon

1. .3489

ORIGIN

##### Alignment Scores:

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Score:	5848.00	Matches:	1163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-830-972-2 (1-1163) x AX766046 (1-3489)

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Qy	21	ProProAlaPheLysTyrGlnPheValThrGluProGluAspGluGluAspGluGluGlu	40
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Qy	41	GluGluAspGluGluGluAspAspGluAspLeuGluGluLeuGluValLeuGluArgLys	60
Db	121	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAAGTGGAGGTGCTGGAGAGGAAG	180
Qy	61	ProAlaAlaGlyLeuSerAlaAlaAlaValProProAlaAlaAlaAlaProLeuLeuAsp	80
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:29:46 ; Search time 1645.69 Seconds  
(without alignments)  
4183.459 Million cell updates/sec

Title: US-09-830-972-2  
Perfect score: 5848  
Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRKAD 1163

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	5848	100.0	4684	6	ABN86600	Abn86600 Rat neuro
4	5307	90.7	3492	12	ADO07888	Ado07888 Mouse pol
5	4403.5	75.3	3919	12	ADP45550	Adp45550 Human Nog
6	4403.5	75.3	4053	4	AAS09453	Aas09453 Human cDN
7	4403.5	75.3	4053	9	ACC81048	Acc81048 Human Nog
8	4403.5	75.3	4053	12	ADP13574	Adp13574 Renal cel
9	4403.5	75.3	4632	6	ABV94680	Abv94680 Human pan
10	4403.5	75.3	4632	10	ADG32772	Adg32772 Human DNA
11	4403.5	75.3	4789	13	ADR83534	Adr83534 Human ret
12	4398.5	75.2	3579	3	AAZ56886	Aaz56886 Human MAG
13	4398.5	75.2	3579	4	AAF90324	Aaf90324 Human NOG
14	4398.5	75.2	3579	6	ABK90134	Abk90134 DNA encod
15	4398.5	75.2	3579	6	ABN86601	Abn86601 Human neu
16	4398.5	75.2	3579	12	ADO07886	Ado07886 Human pol
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18	4381.5	74.9	4093	3	AAA23454	Aaa23454 cDNA enco
19	4350.5	74.4	4822	6	ABS70449	Abs70449 Human bon
20	4329	74.0	4698	8	ABX34563	Abx34563 Human mdd
21	3834	65.6	2425	12	ADO26412	Ado26412 Rat trunc
22	3584	61.3	2248	12	ADO26411	Ado26411 Rat trunc
23	3575	61.1	2278	12	ADO26413	Ado26413 Rat trunc
24	3495.5	59.8	60615	13	ADT89536	Adt89536 Mus muscu
25	3413	58.4	3833	3	AAD01174	Aad01174 Bovine ne
26	2632.5	45.0	2386	2	AAV30920	Aav30920 Human sec
27	2623.5	44.9	2386	5	AAF98399	Aaf98399 Human cDN
28	1975	33.8	1980	4	AAI98079	Aai98079 Human neu
29	1513	25.9	2782	10	ADB85284	Adb85284 Rat fooce
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31	1191	20.4	1122	4	AAF90325	Aaf90325 Human NOG
32	1191	20.4	1216	6	ABA05903	Aba05903 Human RTN
33	1191	20.4	1599	10	ADI62860	Adi62860 Human apo
34	1191	20.4	1610	3	AAZ36230	Aaz36230 cDNA enco
35	1191	20.4	2235	6	ABV94681	Abv94681 Human pan
36	1191	20.4	2240	3	AAC64406	Aac64406 Human Nog
37	1183	20.2	2052	6	ABK90133	Abk90133 DNA encod
38	1174	20.1	1694	4	AAK94408	Aak94408 Human ful
39	1174	20.1	1694	12	ADL31137	Adl31137 Full leng
40	1035.5	17.7	1683	4	AAD08386	Aad08386 Human sec
41	925	15.8	1568	3	AAD01175	Aad01175 Rat neuro
42	917	15.7	734	12	ADF42781	Adf42781 Mouse CYP
c 43	916.5	15.7	1758	4	AAF32725	Aaf32725 Human sec
44	911.5	15.6	2100	8	ABT42936	Abt42936 Human neu

## ALIGNMENTS

## RESULT 1

ADP45571

ID ADP45571 standard; cDNA; 3492 BP.

XX

AC ADP45571;

XX

DT 09-SEP-2004 (first entry)

XX

DE Rat NogoA encoding cDNA SEQ ID NO:25.

XX

KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;

KW nerve repair; neuroprotective; gene therapy;

KW central nervous system injury; CNS injury; neurodegenerative disorder;

KW rat; gene; ss.

XX

OS Rattus norvegicus.

XX

FH Key Location/Qualifiers

FT CDS 1..3492

FT /\*tag= a

FT /product= "NogoA"

XX

PN WO2004052932-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-EP013960.

XX

PR 10-DEC-2002; 2002GB-00028832.

XX

PA (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS PHARMA GMBH.

PA (UYZU-) UNIV ZUERICH.

XX

PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

PI Zurini M;

XX

DR WPI; 2004-468818/44.

DR P-PSDB; ADP45572.

XX

PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-

PT D20 or NogoA623-640, useful in preparing a composition for treating CNS

PT injury or neurodegenerative disorders.

XX

PS Disclosure; SEQ ID NO 25; 121pp; English.

XX

CC The present invention describes a binding molecule which binds to human  
CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a  
CC dissociation constant of less than 1000nM. Also described: (1) a  
CC polynucleotide encoding the binding molecule; (2) an expression vector or  
CC system comprising the polynucleotide; (3) a host cell comprising the  
CC expression system; (4) a pharmaceutical composition comprising the

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:35:57 ; Search time 507.898 Seconds  
(without alignments)  
3746.799 Million cell updates/sec

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Perfect score: 5848  
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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.



## SUMMARIES

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	3	908	15.5	1669	4	US-09-949-016-3253	Sequence 3253, Ap
	4	895	15.3	2610	4	US-09-023-655-382	Sequence 382, App
	5	797.5	13.6	3202	4	US-09-949-016-1127	Sequence 1127, Ap
	6	741.5	12.7	3517	4	US-09-799-451-111	Sequence 111, App
	7	724.5	12.4	2069	4	US-09-949-016-3309	Sequence 3309, Ap
	8	625.5	10.7	1766	3	US-09-149-476-254	Sequence 254, App
	9	625.5	10.7	2262	4	US-09-949-016-2988	Sequence 2988, Ap
	10	625.5	10.7	2664	3	US-09-149-476-255	Sequence 255, App
	11	527.5	9.0	1095	2	US-08-700-607-4	Sequence 4, Appli
	12	522.5	8.9	2014	4	US-09-270-767-13561	Sequence 13561, A
	13	518.5	8.9	794	3	US-09-149-476-102	Sequence 102, App
	14	490	8.4	2181	4	US-09-949-016-1419	Sequence 1419, Ap
	15	444.5	7.6	428	4	US-09-513-999C-923	Sequence 923, App
	16	345	5.9	382	4	US-09-513-999C-11526	Sequence 11526, A
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c	18	341	5.8	601	4	US-09-949-016-117589	Sequence 117589,
	19	341	5.8	42075	4	US-09-949-016-14995	Sequence 14995, A
	20	294.5	5.0	145287	4	US-09-949-016-13530	Sequence 13530, A
	21	294.5	5.0	145287	4	US-09-949-016-13531	Sequence 13531, A
	22	293	5.0	443	4	US-09-513-999C-3784	Sequence 3784, Ap
	23	288	4.9	7571	4	US-09-949-016-4366	Sequence 4366, Ap
	24	288	4.9	8146	4	US-09-976-594-725	Sequence 725, App
	25	288	4.9	11917	4	US-09-566-921-32	Sequence 32, Appl
	26	288	4.9	101300	4	US-09-949-016-16108	Sequence 16108, A
	27	286	4.9	441	4	US-09-513-999C-2227	Sequence 2227, Ap
	28	285	4.9	135667	4	US-09-949-016-15051	Sequence 15051, A
	29	285	4.9	152486	4	US-09-949-016-12869	Sequence 12869, A
	30	282.5	4.8	4148	4	US-09-344-624-2	Sequence 2, Appli
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c	32	279.5	4.8	601	4	US-09-949-016-119335	Sequence 119335,
	33	279.5	4.8	5361	3	US-08-973-462-2	Sequence 2, Appli
	34	279.5	4.8	6152	3	US-08-973-462-1	Sequence 1, Appli
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	38	271	4.6	13906	4	US-09-949-016-14730	Sequence 14730, A
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	44	263.5	4.5	4484	4	US-09-949-016-4498	Sequence 4498, Ap
c	45	257	4.4	2835	3	US-09-134-001C-1515	Sequence 1515, Ap

## ALIGNMENTS

RESULT 1  
US-09-484-970B-106

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 22:42:49 ; Search time 1786.79 Seconds  
(without alignments)  
3948.747 Million cell updates/sec

Title: US-09-830-972-2  
Perfect score: 5848  
Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRKAD 1163

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
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6: /cg2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	5848	100.0	4684	9	US-09-893-348-17	Sequence 17, Appl
2	5848	100.0	4684	18	US-10-810-653-17	Sequence 17, Appl
3	5307	90.7	3492	17	US-10-267-502-214	Sequence 214, App
4	4403.5	75.3	4053	9	US-09-758-140-5	Sequence 5, Appli
5	4403.5	75.3	4053	9	US-09-972-599A-5	Sequence 5, Appli
6	4403.5	75.3	4053	18	US-10-717-597-310	Sequence 310, App
7	4403.5	75.3	4632	14	US-10-060-036-53	Sequence 53, Appl
8	4398.5	75.2	3579	9	US-09-789-386-1	Sequence 1, Appli
9	4398.5	75.2	3579	9	US-09-893-348-22	Sequence 22, Appl
10	4398.5	75.2	3579	17	US-10-267-502-212	Sequence 212, App
11	4398.5	75.2	3579	18	US-10-327-213-8	Sequence 8, Appli
12	4398.5	75.2	3579	18	US-10-466-258-8	Sequence 8, Appli
13	4398.5	75.2	3579	18	US-10-810-653-22	Sequence 22, Appl
14	3495.5	59.8	60615	18	US-10-633-423-9	Sequence 9, Appli
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16	1975	33.8	1980	17	US-10-220-891-22	Sequence 22, Appl
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19	1191	20.4	1610	9	US-09-765-205-5	Sequence 5, Appli
20	1191	20.4	2235	14	US-10-060-036-54	Sequence 54, Appl
21	1183	20.2	2052	18	US-10-466-258-3	Sequence 3, Appli
22	911.5	15.6	2100	19	US-10-479-081-217	Sequence 217, App
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24	908	15.5	1160	14	US-10-175-523-156	Sequence 156, App
25	908	15.5	1785	17	US-10-439-388-62	Sequence 62, Appl
26	899	15.4	994	11	US-09-978-360A-110	Sequence 110, App
27	895	15.3	2610	17	US-10-641-643-382	Sequence 382, App
28	888	15.2	868	9	US-09-789-386-3	Sequence 3, Appli
29	868	14.8	1798	18	US-10-466-258-10	Sequence 10, Appl
30	844	14.4	1514	9	US-09-823-245A-349	Sequence 349, App
31	797.5	13.6	3202	9	US-09-954-456-210	Sequence 210, App
32	797.5	13.6	3202	17	US-10-172-118-386	Sequence 386, App
33	797.5	13.6	3202	17	US-10-342-887-386	Sequence 386, App
34	797.5	13.6	3202	18	US-10-723-860-1480	Sequence 1480, Ap
35	797.5	13.6	3202	19	US-10-843-641A-3237	Sequence 3237, Ap

36	797.5	13.6	3305	18	US-10-723-860-5926	Sequence 5926, Ap
37	792	13.5	2343	17	US-10-267-502-215	Sequence 215, App
38	789.5	13.5	2331	17	US-10-267-502-213	Sequence 213, App
39	741.5	12.7	3517	17	US-10-302-172-111	Sequence 111, App
40	713	12.2	3637	17	US-10-108-260A-449	Sequence 449, App
41	713	12.2	3637	17	US-10-159-563-443	Sequence 443, App
42	686.5	11.7	1502	15	US-10-205-219-94	Sequence 94, Appl
43	686	11.7	1520	15	US-10-084-817-333	Sequence 333, App
44	675	11.5	422	9	US-09-960-352-8477	Sequence 8477, Ap
45	671	11.5	1473	15	US-10-205-194-128	Sequence 128, App

#### ALIGNMENTS

#### RESULT 1

US-09-893-348-17

; Sequence 17, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 4684

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (253)..(3744)

; OTHER INFORMATION:

US-09-893-348-17

*Parents don't  
disclose*

#### Alignment Scores:

Pred. No.:	0	Length:	4684
Score:	5848.00	Matches:	1163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:34:27 ; Search time 10281.6 Seconds  
(without alignments)  
4305.640 Million cell updates/sec

Title: US-09-830-972-2  
Perfect score: 5848  
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Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1286.5	22.0	3533	3	AK034902	AK034902	Mus muscu
3	1271	21.7	785	6	CA511870	CA511870	UI-R-FJ0-
4	1258.5	21.5	896	6	CB204418	CB204418	AGENCOURT
5	1255	21.5	842	5	BU709149	BU709149	UI-M-EW0-
6	1220.5	20.9	986	5	BU841009	BU841009	AGENCOURT
7	1218.5	20.8	805	4	BI730192	BI730192	603349739
c 8	1215	20.8	796	6	CA504729	CA504729	UI-R-FJ0-
9	1198	20.5	822	6	CB521332	CB521332	UI-M-GH0-
10	1180.5	20.2	803	7	CN539361	CN539361	UI-M-HU0-
11	1163	19.9	777	6	CA320618	CA320618	UI-M-FW0-
12	1131	19.3	778	5	BU709106	BU709106	UI-M-EW0-
13	1124.5	19.2	772	7	CF948588	CF948588	UI-M-HJ0-
14	1122.5	19.2	802	6	CA320635	CA320635	UI-M-FW0-
15	1121	19.2	756	7	CK635939	CK635939	UI-M-HN0-
16	1114.5	19.1	951	5	BQ892001	BQ892001	AGENCOURT
17	1110.5	19.0	1024	7	CN643847	CN643847	ILLUMIGEN
18	1107	18.9	1013	7	CN646105	CN646105	ILLUMIGEN
19	1097	18.8	638	6	CB576696	CB576696	AMGNNUC:C
20	1094	18.7	862	1	AU079375	AU079375	AU079375
21	1084.5	18.5	739	5	BU612951	BU612951	UI-M-FR0-
22	1080.5	18.5	767	7	CF726835	CF726835	UI-M-HB0-
23	1080	18.5	714	7	CN532333	CN532333	UI-M-HQ0-
24	1077.5	18.4	747	7	CO424137	CO424137	UI-M-HU0-
25	1074	18.4	726	7	CF737320	CF737320	UI-M-HD0-
26	1068.5	18.3	935	5	BQ963057	BQ963057	AGENCOURT
27	1063	18.2	724	7	CF729503	CF729503	UI-M-HD0-
28	1062	18.2	719	7	CN528062	CN528062	UI-M-HQ0-
29	1051.5	18.0	742	6	CA320833	CA320833	UI-M-FW0-
30	1051.5	18.0	844	6	CB845105	CB845105	M2PN-0675
31	1043.5	17.8	714	7	CN456178	CN456178	UI-M-HN0-
32	1043	17.8	700	4	BI664179	BI664179	603289106
33	1041	17.8	779	6	CB244702	CB244702	UI-M-FY0-
34	1039	17.8	688	7	CF540092	CF540092	UI-M-EX0-
35	1023	17.5	673	6	CD349457	CD349457	UI-M-FY0-
36	1021.5	17.5	710	7	CN458728	CN458728	UI-M-HB0-
37	1017	17.4	871	5	BQ719894	BQ719894	AGENCOURT
38	1012	17.3	779	7	CO401465	CO401465	AGENCOURT
39	1004	17.2	751	6	CA315995	CA315995	UI-M-FW0-
40	1001.5	17.1	691	5	BU707644	BU707644	UI-M-FR0-
41	1000.5	17.1	782	4	BI739239	BI739239	603359521
42	997	17.0	609	6	CB580803	CB580803	AMGNNUC:N
43	995	17.0	651	7	CK619609	CK619609	mk26b12.y
44	983	16.8	730	4	BI601346	BI601346	603245090
45	977.5	16.7	683	7	CN526355	CN526355	UI-M-HN0-

# ALIGNMENTS

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 14, 2005, 17:00:28 ; Search time 5390.01 Seconds  
(without alignments)  
3236.333 Million cell updates/sec

Title: SEQ2  
Perfect score: 1823  
Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRKAD 360

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
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FUSION/runat\_14042005\_104546\_4009/app\_query.fasta\_1.1038  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
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-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
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-USER=NICHOLS-09-830-672-FUSION @CGN\_1\_1\_6287 @runat\_14042005\_104546\_4009  
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Database : GenEmbl:\*  
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2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*

12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	1817	99.7	2156	10	AY164740	AY164740 Rattus no
2	1817	99.7	2156	10	RNO242962	AJ242962 Rattus no
3	1817	99.7	2410	10	BC070879	BC070879 Rattus no
4	1800.5	98.8	2782	6	AX700396	AX700396 Sequence
5	1800.5	98.8	2782	10	AY164741	AY164741 Rattus no
6	1800.5	98.8	2782	10	AF132045	AF132045 Rattus no
7	1797	98.6	2256	10	AF132046	AF132046 Rattus no
8	1720	94.3	2209	10	AY102281	AY102281 Mus muscu
9	1709.5	93.8	1276	10	AY114153	AY114153 Mus muscu
10	1703.5	93.4	2266	10	AY102282	AY102282 Mus muscu
11	1596.5	87.6	1122	6	BD249448	BD249448 Protein s
12	1596.5	87.6	1122	9	HSA251384	AJ251384 Homo sapi
13	1596.5	87.6	1485	9	BC010737	BC010737 Homo sapi
14	1596.5	87.6	1599	6	CQ769577	CQ769577 Sequence
15	1596.5	87.6	1610	6	BD231889	BD231889 Bone marr
16	1596.5	87.6	1619	9	AK129806	AK129806 Homo sapi
17	1596.5	87.6	1654	9	BC012619	BC012619 Homo sapi
18	1596.5	87.6	1668	9	BC026788	BC026788 Homo sapi
19	1596.5	87.6	1709	9	AB040463	AB040463 Homo sapi
20	1596.5	87.6	1728	9	BC068991	BC068991 Homo sapi
21	1596.5	87.6	2235	9	AF148538	AF148538 Homo sapi
22	1596.5	87.6	2276	9	AF132047	AF132047 Homo sapi
23	1596.5	87.6	2332	9	AY102277	AY102277 Homo sapi
24	1593.5	87.4	1525	9	AK130812	AK130812 Homo sapi
25	1588.5	87.1	2052	9	AB015639	AB015639 Homo sapi
26	1584	86.9	1784	9	BC016165	BC016165 Homo sapi
27	1584	86.9	2389	9	AY102278	AY102278 Homo sapi
28	1579.5	86.6	1694	6	CQ783030	CQ783030 Sequence
29	1579.5	86.6	1694	6	BD127437	BD127437 Primer fo
30	1579.5	86.6	1694	9	AK075039	AK075039 Homo sapi
31	1469	80.6	1466	9	BC071848	BC071848 Homo sapi
32	1411.5	77.4	3489	6	AX766046	AX766046 Sequence
33	1411.5	77.4	3492	6	CQ829507	CQ829507 Sequence
34	1411.5	77.4	4684	10	RNO242961	AJ242961 Rattus no
35	1313	72.0	4518	10	BC056373	BC056373 Mus muscu
36	1313	72.0	4627	10	AY102284	AY102284 Mus muscu
37	1298.5	71.2	3821	10	AY114152	AY114152 Mus muscu
38	1184	64.9	3576	6	AX766050	AX766050 Sequence
39	1184	64.9	3579	6	BD249446	BD249446 Protein s
40	1184	64.9	3579	9	HSA251383	AJ251383 Homo sapi
41	1184	64.9	3919	6	CQ829486	CQ829486 Sequence
42	1184	64.9	4053	6	AX195249	AX195249 Sequence
43	1184	64.9	4053	9	AB020693	AB020693 Homo sapi
44	1184	64.9	4166	9	AB040462	AB040462 Homo sapi



## ALIGNMENTS

## RESULT 1

AY164740

LOCUS AY164740 2156 bp mRNA linear ROD 30-JUN-2003

DEFINITION Rattus norvegicus RTN4-B1 (Rtn4) mRNA, complete cds; alternatively spliced.

ACCESSION AY164740

VERSION AY164740.1 GI:32331280

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 2156)

AUTHORS Oertle,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.

TITLE A reticular rhapsody: phylogenic evolution and nomenclature of the RTN/Nogo gene family

JOURNAL FASEB J. 17 (10), 1238-1247 (2003)

PUBMED 12832288

REFERENCE 2 (bases 1 to 2156)

AUTHORS Oertle,T. and Schwab,M.E.

TITLE Direct Submission

JOURNAL Submitted (16-OCT-2002) Brain Research Institute and Department Biology, University of Zurich and ETH Zurich, Winterthurerstr.190, Zurich 8057, Switzerland

FEATURES Location/Qualifiers

source

1. .2156  
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/mol\_type="mRNA"  
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gene

1. .2156  
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5'UTR

1. .188  
/gene="Rtn4"

CDS

189. .1271  
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TISFRIYKGVIAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR  
LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYL  
GLANKSVKDAMAKIQAKIPGLKRKAD"

3'UTR

1272. .2156  
/gene="Rtn4"

ORIGIN

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 14, 2005, 15:51:07 ; Search time 646.602 Seconds  
(without alignments)  
3295.856 Million cell updates/sec

Title: SEQ2  
Perfect score: 1823  
Sequence: 1 MEDIDQSSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRKAD 360

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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FUSION/runat\_14042005\_104545\_3999/app\_query.fasta 1.1038  
-DB=N\_Geneseq\_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=NICHOLS-09-830-672-FUSION\_@CGN\_1\_1\_796\_@runat\_14042005\_104545\_3999  
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1800.5	98.8	2782	10	ADB85284	Adb85284 Rat fooce
2	1596.5	87.6	1122	3	AAZ56888	Aaz56888 Human MAG
3	1596.5	87.6	1122	4	AAF90325	Aaf90325 Human NOG
4	1596.5	87.6	1216	6	ABA05903	Aba05903 Human RTN
5	1596.5	87.6	1599	10	ADI62860	Adi62860 Human apo
6	1596.5	87.6	1610	3	AAZ36230	Aaz36230 cDNA enco
7	1596.5	87.6	2235	6	ABV94681	Abv94681 Human pan
8	1596.5	87.6	2240	3	AAC64406	Aac64406 Human Nog
9	1588.5	87.1	2052	6	ABK90133	Abk90133 DNA encod
10	1579.5	86.6	1694	4	AAK94408	Aak94408 Human ful
11	1579.5	86.6	1694	12	ADL31137	Adl31137 Full leng
12	1441	79.0	1683	4	AAD08386	Aad08386 Human sec
13	1411.5	77.4	3492	12	ADP45571	Adp45571 Rat NogoA
14	1411.5	77.4	4684	3	AAD01173	Aad01173 Rat neur
15	1411.5	77.4	4684	6	ABN86600	Abn86600 Rat neuro
16	1298.5	71.2	3492	12	ADO07888	Ado07888 Mouse pol
17	1184	64.9	3579	3	AAZ56886	Aaz56886 Human MAG
18	1184	64.9	3579	4	AAF90324	Aaf90324 Human NOG
19	1184	64.9	3579	6	ABK90134	Abk90134 DNA encod
20	1184	64.9	3579	6	ABN86601	Abn86601 Human neu
21	1184	64.9	3579	12	ADO07886	Ado07886 Human pol
22	1184	64.9	3579	12	ADR13965	Adr13965 Human NOG
23	1184	64.9	3919	12	ADP45550	Adp45550 Human Nog
24	1184	64.9	4053	4	AAS09453	Aas09453 Human cDN
25	1184	64.9	4053	9	ACC81048	Acc81048 Human Nog
26	1184	64.9	4053	12	ADP13574	Adp13574 Renal cel
27	1184	64.9	4632	6	ABV94680	Abv94680 Human pan
28	1184	64.9	4632	10	ADG32772	Adg32772 Human DNA
29	1184	64.9	4789	13	ADR83534	Adr83534 Human ret
30	1170.5	64.2	4093	3	AAA23454	Aaa23454 cDNA enco
31	1169.5	64.2	4822	6	ABS70449	Abs70449 Human bon
32	1161.5	63.7	4698	8	ABX34563	Abx34563 Human mdd
c 33	996.5	54.7	1758	4	AAF32725	Aaf32725 Human sec
34	989	54.3	2934	12	ADQ16433	Adq16433 Construct
35	952	52.2	3833	3	AAD01174	Aad01174 Bovine ne
36	921	50.5	1568	3	AAD01175	Aad01175 Rat neur
37	913	50.1	734	12	ADF42781	Adf42781 Mouse CYP
38	909	49.9	1980	4	AAI98079	Aai98079 Human neu
39	904	49.6	600	4	AAF90323	Aaf90323 Human NOG
40	904	49.6	770	3	AAA72983	Aaa72983 Human NSP
41	904	49.6	799	2	AAV23695	Aav23695 Human NSP
42	904	49.6	1213	2	AAX04379	Aax04379 Human sec
43	904	49.6	1785	12	ADK14166	Adk14166 Human aut
44	895	49.1	991	2	AAX97587	Aax97587 Extended
45	895	49.1	994	12	ADP18854	Adp18854 Human sec

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 14, 2005, 20:35:54 ; Search time 434.896 Seconds  
(without alignments)  
1354.484 Million cell updates/sec

Title: SEQ2  
Perfect score: 1823  
Sequence: 1 MEDIDQSSILVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRKAD 360

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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	No.	Score	Query Match	Length	DB	ID	
	1	1169.5	64.2	4822	3	US-09-484-970B-106	Sequence 106, App
	2	904	49.6	799	2	US-08-700-607-2	Sequence 2, Appli
	3	904	49.6	1669	4	US-09-949-016-3253	Sequence 3253, Ap
	4	891	48.9	2610	4	US-09-023-655-382	Sequence 382, App
	5	773	42.4	2069	4	US-09-949-016-3309	Sequence 3309, Ap
	6	773	42.4	3202	4	US-09-949-016-1127	Sequence 1127, Ap
	7	678.5	37.2	1766	3	US-09-149-476-254	Sequence 254, App
	8	673.5	36.9	2664	3	US-09-149-476-255	Sequence 255, App
	9	625.5	34.3	2262	4	US-09-949-016-2988	Sequence 2988, Ap
	10	568.5	31.2	1095	2	US-08-700-607-4	Sequence 4, Appli
	11	558.5	30.6	794	3	US-09-149-476-102	Sequence 102, App
	12	547	30.0	3517	4	US-09-799-451-111	Sequence 111, App
	13	522.5	28.7	2181	4	US-09-949-016-1419	Sequence 1419, Ap
	14	522	28.6	2014	4	US-09-270-767-13561	Sequence 13561, A
c	15	341	18.7	601	4	US-09-949-016-117588	Sequence 117588,
c	16	341	18.7	601	4	US-09-949-016-117589	Sequence 117589,
	17	341	18.7	42075	4	US-09-949-016-14995	Sequence 14995, A
	18	302	16.6	443	4	US-09-513-999C-3784	Sequence 3784, Ap
	19	286	15.7	441	4	US-09-513-999C-2227	Sequence 2227, Ap
	20	284	15.6	135667	4	US-09-949-016-15051	Sequence 15051, A
	21	284	15.6	152486	4	US-09-949-016-12869	Sequence 12869, A
c	22	278.5	15.3	601	4	US-09-949-016-40169	Sequence 40169, A
c	23	278.5	15.3	601	4	US-09-949-016-119335	Sequence 119335,
	24	276	15.1	261	2	US-08-700-607-9	Sequence 9, Appli
	25	271	14.9	13906	4	US-09-949-016-14730	Sequence 14730, A
	26	262	14.4	15661	4	US-09-949-016-13161	Sequence 13161, A
	27	256.5	14.1	454	4	US-09-621-976-740	Sequence 740, App
	28	256.5	14.1	463	4	US-09-621-976-741	Sequence 741, App
	29	243	13.3	200	4	US-09-513-999C-11198	Sequence 11198, A
	30	209.5	11.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	31	209.5	11.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	32	208	11.4	2580	3	US-09-050-863-2	Sequence 2, Appli
c	33	208	11.4	2580	3	US-09-359-081-2	Sequence 2, Appli
	34	208	11.4	8705	4	US-09-647-344A-14	Sequence 14, Appl
c	35	208	11.4	9600	3	US-08-910-647-1	Sequence 1, Appli
c	36	208	11.4	9600	3	US-09-620-925-1	Sequence 1, Appli
c	37	208	11.4	10596	1	US-07-884-811-15	Sequence 15, Appl
c	38	208	11.4	10596	1	US-07-885-971-15	Sequence 15, Appl
c	39	208	11.4	10596	1	US-08-087-783A-15	Sequence 15, Appl
c	40	208	11.4	10596	1	US-08-194-088B-15	Sequence 15, Appl
c	41	208	11.4	10596	2	US-08-194-087-15	Sequence 15, Appl
c	42	208	11.4	10596	5	PCT-US93-04648-15	Sequence 15, Appl
	43	208	11.4	16080	4	US-09-724-566A-48	Sequence 48, Appl
	44	208	11.4	16080	4	US-09-471-669A-48	Sequence 48, Appl
c	45	207.5	11.4	1926	3	US-09-249-585A-2	Sequence 2, Appli

## ALIGNMENTS

## RESULT 1

US-09-484-970B-106

; Sequence 106, Application US/09484970B

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 15, 2005, 00:27:04 ; Search time 1596.28 Seconds  
(without alignments)  
1368.189 Million cell updates/sec

Title: SEQ2  
Perfect score: 1823  
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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
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5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1800.5	98.8	2782	15	US-10-205-194-165	Sequence 165, App	
2	1596.5	87.6	1122	9		Sequence 5, Appli	
3	1596.5	87.6	1610	9	US-09-765-205-5	Sequence 5, Appli	
4	1596.5	87.6	2235	14	US-10-060-036-54	Sequence 54, Appl	
5	1588.5	87.1	2052	18	US-10-466-258-3	Sequence 3, Appli	
6	1411.5	77.4	4684	9	US-09-893-348-17	Sequence 17, Appl	
7	1411.5	77.4	4684	18	US-10-810-653-17	Sequence 17, Appl	
8	1298.5	71.2	3492	17	US-10-267-502-214	Sequence 214, App	
9	1184	64.9	3579	9	US-09-789-386-1	Sequence 1, Appli	
10	1184	64.9	3579	9	US-09-893-348-22	Sequence 22, Appl	
11	1184	64.9	3579	17	US-10-267-502-212	Sequence 212, App	
12	1184	64.9	3579	18	US-10-327-213-8	Sequence 8, Appli	
13	1184	64.9	3579	18	US-10-466-258-8	Sequence 8, Appli	
14	1184	64.9	3579	18	US-10-810-653-22	Sequence 22, Appl	
15	1184	64.9	4053	9	US-09-758-140-5	Sequence 5, Appli	
16	1184	64.9	4053	9	US-09-972-599A-5	Sequence 5, Appli	
17	1184	64.9	4053	18	US-10-717-597-310	Sequence 310, App	
18	1184	64.9	4632	14	US-10-060-036-53	Sequence 53, Appl	
19	909	49.9	1980	17	US-10-220-891-22	Sequence 22, Appl	
20	904	49.6	799	17	US-10-660-946-2	Sequence 2, Appli	
21	904	49.6	1160	14	US-10-175-523-156	Sequence 156, App	
22	904	49.6	1785	17	US-10-439-388-62	Sequence 62, Appl	
23	895	49.1	994	11	US-09-978-360A-110	Sequence 110, App	
24	891	48.9	2610	17	US-10-641-643-382	Sequence 382, App	
25	864	47.4	1798	18	US-10-466-258-10	Sequence 10, Appl	
26	844	46.3	1514	9	US-09-823-245A-349	Sequence 349, App	
27	809	44.4	60615	18	US-10-633-423-9	Sequence 9, Appli	
28	809	44.4	60615	18	US-10-427-741-9	Sequence 9, Appli	
29	774	42.5	2343	17	US-10-267-502-215	Sequence 215, App	
30	773	42.4	2331	17	US-10-267-502-213	Sequence 213, App	
31	773	42.4	3202	9	US-09-954-456-210	Sequence 210, App	
32	773	42.4	3202	17	US-10-172-118-386	Sequence 386, App	
33	773	42.4	3202	17	US-10-342-887-386	Sequence 386, App	
34	773	42.4	3202	18	US-10-723-860-1480	Sequence 1480, Ap	
35	773	42.4	3202	19	US-10-843-641A-3237	Sequence 3237, Ap	

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38	696	38.2	1520	15	US-10-084-817-333	Sequence 333, App
39	686	37.6	1473	15	US-10-205-194-128	Sequence 128, App
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41	678.5	37.2	1766	10	US-09-882-171-254	Sequence 254, App
42	678.5	37.2	1766	17	US-10-164-861-254	Sequence 254, App
43	675	37.0	422	9	US-09-960-352-8477	Sequence 8477, Ap
44	673.5	36.9	2664	10	US-09-809-391-255	Sequence 255, App
45	673.5	36.9	2664	10	US-09-882-171-255	Sequence 255, App

# ALIGNMENTS

## RESULT 1

US-10-205-194-165

; Sequence 165, Application US/10205194

; Publication No. US20030134301A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert Company

; APPLICANT: Lee, Kevin

; APPLICANT: Dixon, Alistair

; APPLICANT: Brooksbank, Robert

; APPLICANT: Pinnock, Robert

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

; FILE REFERENCE: WL-A-018201

; CURRENT APPLICATION NUMBER: US/10/205,194

; CURRENT FILING DATE: 5200-07-24

; PRIOR APPLICATION NUMBER: GB 0118354.0

; PRIOR FILING DATE: 2001-07-27

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 165

; LENGTH: 2782

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; OTHER INFORMATION: Foocen-m2 reticulon

US-10-205-194-165

## Alignment Scores:

Pred. No.:	3.27e-150	Length:	2782
Score:	1800.50	Matches:	359
Percent Similarity:	94.99%	Conservative:	1
Best Local Similarity:	94.72%	Mismatches:	0
Query Match:	98.77%	Indels:	19
DB:	15	Gaps:	1

SEQ2 (1-360) x US-10-205-194-165 (1-2782)

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Db	761	CCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCCGAGGACGAGGAGGACGAGGAGGAG	820



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 14, 2005, 17:27:17 ; Search time 3995.95 Seconds  
(without alignments)  
3429.256 Million cell updates/sec

Title: SEQ2  
Perfect score: 1823  
Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRKAD 360

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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3: gb\_htc: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	% Query						Description
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	1	1692	92.8	3533	3	AK034902	AK034902 Mus muscu
	2	1244	68.2	781	4	BI079496	BI079496 602876306
	3	1084	59.5	810	4	BI080232	BI080232 602876650
	4	1056.5	58.0	1097	5	BX439214	BX439214 BX439214
	5	1006	55.2	708	4	BI157842	BI157842 602923001
	6	985	54.0	815	2	BF099705	BF099705 601751340
	7	973.5	53.4	911	1	AL549191	AL549191 AL549191
	8	967.5	53.1	924	5	BU845601	BU845601 AGENCOURT
	9	966	53.0	677	7	CN791158	CN791158 4125836 B
	10	965	52.9	990	4	BI691132	BI691132 603314519
	11	940	51.6	679	4	BI149602	BI149602 602848410
	12	939	51.5	592	7	CN482802	CN482802 hw24h12.y
	13	928	50.9	779	7	CO401465	CO401465 AGENCOURT
	14	921	50.5	695	7	CV077130	CV077130 AGENCOURT
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	16	917	50.3	598	7	CF118424	CF118424 fs543.z1
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	19	912.5	50.1	667	7	CN429712	CN429712 170006000
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	24	907	49.8	799	1	AU080133	AU080133 AU080133
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	29	904	49.6	758	4	BG697436	BG697436 602660623
	30	904	49.6	788	1	AL533461	AL533461 AL533461
	31	904	49.6	843	4	BG570231	BG570231 602590632
	32	904	49.6	849	7	CR765672	CR765672 DKFZp469C
c	33	904	49.6	875	1	AL573494	AL573494 AL573494
	34	904	49.6	1540	3	CR611869	CR611869 full-leng
	35	904	49.6	1785	3	AF077050	AF077050 Homo sapi
	36	901	49.4	730	1	AU297347	AU297347 AU297347
	37	898	49.3	634	6	CB067821	CB067821 iq38a06.y
	38	898	49.3	670	7	CV030029	CV030029 9024 Full
	39	898	49.3	960	7	CN646472	CN646472 ILLUMIGEN
	40	898	49.3	983	7	CN803408	CN803408 ILLUMIGEN
	41	898	49.3	1031	7	CN647521	CN647521 ILLUMIGEN
	42	894	49.0	751	7	CK357937	CK357937 AGENCOURT
	43	893	49.0	718	1	AA986233	AA986233 uc73gl2.y
	44	892	48.9	805	7	CO735185	CO735185 S1LE04c10
	45	891	48.9	749	4	BG296048	BG296048 602393712

# ALIGNMENTS

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 14, 2005, 17:00:28 ; Search time 5404.99 Seconds  
(without alignments)  
3236.333 Million cell updates/sec

Title: SEQ29  
Perfect score: 1850  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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FUSION/runat\_14042005\_104546\_4009/app\_query.fasta\_1.1038  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*

12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1829	98.9	1122	6	BD249448	BD249448 Protein s
2	1829	98.9	1122	9	HSA251384	AJ251384 Homo sapi
3	1829	98.9	1485	9	BC010737	BC010737 Homo sapi
4	1829	98.9	1610	6	BD231889	BD231889 Bone marr
5	1829	98.9	1619	9	AK129806	AK129806 Homo sapi
6	1829	98.9	1654	9	BC012619	BC012619 Homo sapi
7	1829	98.9	1668	9	BC026788	BC026788 Homo sapi
8	1829	98.9	1709	9	AB040463	AB040463 Homo sapi
9	1829	98.9	1728	9	BC068991	BC068991 Homo sapi
10	1829	98.9	2235	9	AF148538	AF148538 Homo sapi
11	1829	98.9	2276	9	AF132047	AF132047 Homo sapi
12	1829	98.9	2332	9	AY102277	AY102277 Homo sapi
13	1826	98.7	1525	9	AK130812	AK130812 Homo sapi
14	1825	98.6	1599	6	CQ769577	CQ769577 Sequence
15	1821.5	98.5	1784	9	BC016165	BC016165 Homo sapi
16	1821.5	98.5	2389	9	AY102278	AY102278 Homo sapi
17	1821	98.4	2052	9	AB015639	AB015639 Homo sapi
18	1812	97.9	1694	6	CQ783030	CQ783030 Sequence
19	1812	97.9	1694	6	BD127437	BD127437 Primer fo
20	1812	97.9	1694	9	AK075039	AK075039 Homo sapi
21	1667	90.1	1466	9	BC071848	BC071848 Homo sapi
22	1545	83.5	2782	6	AX700396	AX700396 Sequence
23	1545	83.5	2782	10	AY164741	AY164741 Rattus no
24	1545	83.5	2782	10	AF132045	AF132045 Rattus no
25	1537.5	83.1	2156	10	AY164740	AY164740 Rattus no
26	1537.5	83.1	2156	10	RNO242962	AJ242962 Rattus no
27	1537.5	83.1	2410	10	BC070879	BC070879 Rattus no
28	1521.5	82.2	2256	10	AF132046	AF132046 Rattus no
29	1521	82.2	2266	10	AY102282	AY102282 Mus muscu
30	1513.5	81.8	2209	10	AY102281	AY102281 Mus muscu
31	1503	81.2	1276	10	AY114153	AY114153 Mus muscu
32	1424.5	77.0	3576	6	AX766050	AX766050 Sequence
33	1424.5	77.0	3579	6	BD249446	BD249446 Protein s
34	1424.5	77.0	3579	9	HSA251383	AJ251383 Homo sapi
35	1424.5	77.0	3919	6	CQ829486	CQ829486 Sequence
36	1424.5	77.0	4053	6	AX195249	AX195249 Sequence
37	1424.5	77.0	4053	9	AB020693	AB020693 Homo sapi
38	1424.5	77.0	4166	9	AB040462	AB040462 Homo sapi
39	1424.5	77.0	4632	9	AF148537	AF148537 Homo sapi
40	1424.5	77.0	4789	6	CQ874017	CQ874017 Sequence
41	1424.5	77.0	4789	9	AY102279	AY102279 Homo sapi
42	1401	75.7	4093	6	BD270070	BD270070 Secreted
43	1396	75.5	4822	6	AR220865	AR220865 Sequence
44	1220.5	66.0	2934	6	CQ828004	CQ828004 Sequence

## ALIGNMENTS

## RESULT 1

BD249448

LOCUS BD249448 1122 bp DNA linear PAT 17-JUL-2003

DEFINITION Protein similar to neuroendocrine-specific protein, and encoding cDNA.

ACCESSION BD249448

VERSION BD249448.1 GI:33059218

KEYWORDS JP 2002522016-A/3.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1122)

AUTHORS Michalovich,D. and Prinjha,R.K.

TITLE Protein similar to neuroendocrine-specific protein, and encoding

JOURNAL Patent: JP 2002522016-A 3 23-JUL-2002;

SMITHKLINE BEECHAM PLC

COMMENT OS Homo sapiens (human)

PN JP 2002522016-A/3

PD 23-JUL-2002

PF 21-JUL-1999 JP 2000561310

PR 22-JUL-1998 GB 9816024.5,19-JUL-1999 GB 9916898.1 PI

DAVID MICHALOVICH,RABINDER KUMAR PRINJHA

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC

PC C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC G01N33/566//

PC C12P21/08,C12N15/00,C12N5/00

CC Protein similar to neuroendocrine-specific protein, and encoding cDNA

FH Key Location/Qualifiers

FT source 1. .1122

FT /organism='Homo sapiens (human)'. .

FEATURES Location/Qualifiers

source 1. .1122

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

## Alignment Scores:

Pred. No.:	1.03e-65	Length:	1122
Score:	1829.00	Matches:	360
Percent Similarity:	96.51%	Conservative:	0
Best Local Similarity:	96.51%	Mismatches:	1
Query Match:	98.86%	Indels:	12
DB:	6	Gaps:	1

SEQ29 (1-361) x BD249448 (1-1122)

Qy 1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 14, 2005, 15:51:07 ; Search time 648.398 Seconds  
(without alignments)  
3295.856 Million cell updates/sec

Title: SEQ29  
Perfect score: 1850  
Sequence: 1 MEDLDQSPVLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/NICHOLS-09-830-672-  
FUSION/runat\_14042005\_104545\_3999/app\_query.fasta\_1.1038  
-DB=N\_Geneseq\_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*

12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1829	98.9	1122	3	AAZ56888	Aaz56888 Human MAG
2	1829	98.9	1122	4	AAF90325	Aaf90325 Human NOG
3	1829	98.9	1216	6	ABA05903	Aba05903 Human RTN
4	1829	98.9	1610	3	AAZ36230	Aaz36230 cDNA enco
5	1829	98.9	2235	6	ABV94681	Abv94681 Human pan
6	1829	98.9	2240	3	AAC64406	Aac64406 Human Nog
7	1825	98.6	1599	10	ADI62860	Adi62860 Human apo
8	1821	98.4	2052	6	ABK90133	Abk90133 DNA encod
9	1812	97.9	1694	4	AAK94408	Aak94408 Human ful
10	1812	97.9	1694	12	ADL31137	Adl31137 Full leng
11	1673.5	90.5	1683	4	AAD08386	Aad08386 Human sec
12	1545	83.5	2782	10	ADB85284	Adb85284 Rat fooce
13	1424.5	77.0	3579	3	AAZ56886	Aaz56886 Human MAG
14	1424.5	77.0	3579	4	AAF90324	Aaf90324 Human NOG
15	1424.5	77.0	3579	6	ABK90134	Abk90134 DNA encod
16	1424.5	77.0	3579	6	ABN86601	Abn86601 Human neu
17	1424.5	77.0	3579	12	ADO07886	Ado07886 Human pol
18	1424.5	77.0	3579	12	ADR13965	Adr13965 Human NOG
19	1424.5	77.0	3919	12	ADP45550	Adp45550 Human Nog
20	1424.5	77.0	4053	4	AAS09453	Aas09453 Human cDN
21	1424.5	77.0	4053	9	ACC81048	Acc81048 Human Nog
22	1424.5	77.0	4053	12	ADP13574	Adp13574 Renal cel
23	1424.5	77.0	4632	6	ABV94680	Abv94680 Human pan
24	1424.5	77.0	4632	10	ADG32772	Adg32772 Human DNA
25	1424.5	77.0	4789	13	ADR83534	Adr83534 Human ret
26	1401	75.7	4093	3	AAA23454	Aaa23454 cDNA enco
27	1396	75.5	4822	6	ABS70449	Abs70449 Human bon
28	1392	75.2	4698	8	ABX34563	Abx34563 Human mdd
29	1220.5	66.0	2934	12	ADQ16433	Adq16433 Construct
30	1154	62.4	3492	12	ADP45571	Adp45571 Rat NogoA
31	1154	62.4	4684	3	AAD01173	Aad01173 Rat neuro
32	1154	62.4	4684	6	ABN86600	Abn86600 Rat neuro
33	1114	60.2	3492	12	ADO07888	Ado07888 Mouse pol
c 34	1040.5	56.2	1758	4	AAF32725	Aaf32725 Human sec
35	968.5	52.4	3833	3	AAD01174	Aad01174 Bovine ne
36	942.5	50.9	1980	4	AAI98079	Aai98079 Human neu
37	927	50.1	600	4	AAF90323	Aaf90323 Human NOG
38	927	50.1	770	3	AAA72983	Aaa72983 Human NSP
39	927	50.1	799	2	AAV23695	Aav23695 Human NSP
40	927	50.1	1213	2	AAX04379	Aax04379 Human sec
41	927	50.1	1785	12	ADK14166	Adk14166 Human aut
42	919	49.7	555	12	ADQ16423	Adq16423 Nucleotid
43	918	49.6	991	2	AAX97587	Aax97587 Extended
44	918	49.6	994	12	ADP18854	Adp18854 Human sec
45	916	49.5	2386	2	AAV30920	Aav30920 Human sec

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 14, 2005, 20:35:54 ; Search time 436.104 Seconds  
(without alignments)  
1354.484 Million cell updates/sec

Title: SEQ29  
Perfect score: 1850  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/NICHOLS-09-830-672-  
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-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.



## SUMMARIES

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1	1396	75.5	4822	3	US-09-484-970B-106	Sequence 106, App		
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3	927	50.1	1669	4	US-09-949-016-3253	Sequence 3253, Ap		
4	914	49.4	2610	4	US-09-023-655-382	Sequence 382, App		
5	762	41.2	2069	4	US-09-949-016-3309	Sequence 3309, Ap		
6	762	41.2	3202	4	US-09-949-016-1127	Sequence 1127, Ap		
7	678	36.6	1766	3	US-09-149-476-254	Sequence 254, App		
8	665	35.9	2664	3	US-09-149-476-255	Sequence 255, App		
9	627.5	33.9	2262	4	US-09-949-016-2988	Sequence 2988, Ap		
10	556	30.1	1095	2	US-08-700-607-4	Sequence 4, Appli		
11	554	29.9	3517	4	US-09-799-451-111	Sequence 111, App		
12	548	29.6	794	3	US-09-149-476-102	Sequence 102, App		
13	529	28.6	2181	4	US-09-949-016-1419	Sequence 1419, Ap		
14	518	28.0	2014	4	US-09-270-767-13561	Sequence 13561, A		
15	347	18.8	441	4	US-09-513-999C-2227	Sequence 2227, Ap		
16	344.5	18.6	454	4	US-09-621-976-740	Sequence 740, App		
17	344.5	18.6	463	4	US-09-621-976-741	Sequence 741, App		
c 18	341	18.4	601	4	US-09-949-016-117588	Sequence 117588,		
c 19	341	18.4	601	4	US-09-949-016-117589	Sequence 117589,		
20	341	18.4	42075	4	US-09-949-016-14995	Sequence 14995, A		
21	299	16.2	443	4	US-09-513-999C-3784	Sequence 3784, Ap		
22	284.5	15.4	135667	4	US-09-949-016-15051	Sequence 15051, A		
23	284.5	15.4	152486	4	US-09-949-016-12869	Sequence 12869, A		
c 24	279.5	15.1	601	4	US-09-949-016-40169	Sequence 40169, A		
c 25	279.5	15.1	601	4	US-09-949-016-119335	Sequence 119335,		
26	276	14.9	261	2	US-08-700-607-9	Sequence 9, Appli		
27	271	14.6	13906	4	US-09-949-016-14730	Sequence 14730, A		
28	256	13.8	200	4	US-09-513-999C-11198	Sequence 11198, A		
29	252.5	13.6	15661	4	US-09-949-016-13161	Sequence 13161, A		
c 30	226	12.2	2580	3	US-09-050-863-2	Sequence 2, Appli		
c 31	226	12.2	2580	3	US-09-359-081-2	Sequence 2, Appli		
32	226	12.2	8705	4	US-09-647-344A-14	Sequence 14, Appl		
c 33	226	12.2	9600	3	US-08-910-647-1	Sequence 1, Appli		
c 34	226	12.2	9600	3	US-09-620-925-1	Sequence 1, Appli		
c 35	226	12.2	10596	1	US-07-884-811-15	Sequence 15, Appl		
c 36	226	12.2	10596	1	US-07-885-971-15	Sequence 15, Appl		
c 37	226	12.2	10596	1	US-08-087-783A-15	Sequence 15, Appl		
c 38	226	12.2	10596	1	US-08-194-088B-15	Sequence 15, Appl		
c 39	226	12.2	10596	2	US-08-194-087-15	Sequence 15, Appl		
c 40	226	12.2	10596	5	PCT-US93-04648-15	Sequence 15, Appl		
41	226	12.2	16080	4	US-09-724-566A-48	Sequence 48, Appl		
42	226	12.2	16080	4	US-09-471-669A-48	Sequence 48, Appl		
43	221	11.9	5452	2	US-09-130-114-1	Sequence 1, Appli		
c 44	219	11.8	1926	3	US-09-249-585A-2	Sequence 2, Appli		
c 45	219	11.8	1926	4	US-09-410-399-3	Sequence 3, Appli		

## ALIGNMENTS

## RESULT 1

US-09-484-970B-106

; Sequence 106, Application US/09484970B

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 15, 2005, 00:27:04 ; Search time 1600.72 Seconds  
(without alignments)  
1368.189 Million cell updates/sec

Title: SEQ29  
Perfect score: 1850  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/NICHOLS-09-830-672-  
FUSION/runat\_14042005\_104549\_4109/app\_query.fasta\_1.1038  
-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000  
-USER=NICHOLS-09-830-672-FUSION\_@CGN\_1\_1\_893\_@runat\_14042005\_104549\_4109  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	1829	98.9	1122	9	US-09-789-386-5	Sequence 5, Appli
2	1829	98.9	1610	9	US-09-765-205-5	Sequence 5, Appli
3	1829	98.9	2235	14	US-10-060-036-54	Sequence 54, Appl
4	1821	98.4	2052	18	US-10-466-258-3	Sequence 3, Appli
5	1545	83.5	2782	15	US-10-205-194-165	Sequence 165, App
6	1424.5	77.0	3579	9	US-09-789-386-1	Sequence 1, Appli
7	1424.5	77.0	3579	9	US-09-893-348-22	Sequence 22, Appl
8	1424.5	77.0	3579	17	US-10-267-502-212	Sequence 212, App
9	1424.5	77.0	3579	18	US-10-327-213-8	Sequence 8, Appli
10	1424.5	77.0	3579	18	US-10-466-258-8	Sequence 8, Appli
11	1424.5	77.0	3579	18	US-10-810-653-22	Sequence 22, Appl
12	1424.5	77.0	4053	9	US-09-758-140-5	Sequence 5, Appli
13	1424.5	77.0	4053	9	US-09-972-599A-5	Sequence 5, Appli
14	1424.5	77.0	4053	18	US-10-717-597-310	Sequence 310, App
15	1424.5	77.0	4632	14	US-10-060-036-53	Sequence 53, Appl
16	1154	62.4	4684	9	US-09-893-348-17	Sequence 17, Appl
17	1154	62.4	4684	18	US-10-810-653-17	Sequence 17, Appl
18	1114	60.2	3492	17	US-10-267-502-214	Sequence 214, App
19	942.5	50.9	1980	17	US-10-220-891-22	Sequence 22, Appl
20	927	50.1	799	17	US-10-660-946-2	Sequence 2, Appli
21	927	50.1	1160	14	US-10-175-523-156	Sequence 156, App
22	927	50.1	1785	17	US-10-439-388-62	Sequence 62, Appl
23	918	49.6	994	11	US-09-978-360A-110	Sequence 110, App
24	914	49.4	2610	17	US-10-641-643-382	Sequence 382, App
25	886	47.9	1798	18	US-10-466-258-10	Sequence 10, Appl
26	867	46.9	1514	9	US-09-823-245A-349	Sequence 349, App
27	762	41.2	2331	17	US-10-267-502-213	Sequence 213, App
28	762	41.2	3202	9	US-09-954-456-210	Sequence 210, App
29	762	41.2	3202	17	US-10-172-118-386	Sequence 386, App
30	762	41.2	3202	17	US-10-342-887-386	Sequence 386, App
31	762	41.2	3202	18	US-10-723-860-1480	Sequence 1480, Ap
32	762	41.2	3202	19	US-10-843-641A-3237	Sequence 3237, Ap
33	758.5	41.0	2343	17	US-10-267-502-215	Sequence 215, App
34	755	40.8	3305	18	US-10-723-860-5926	Sequence 5926, Ap
35	715.5	38.7	1502	15	US-10-205-219-94	Sequence 94, Appl

36	703	38.0	1520	15	US-10-084-817-333	Sequence 333, App
37	699	37.8	1473	15	US-10-205-194-128	Sequence 128, App
38	695	37.6	422	9	US-09-960-352-8477	Sequence 8477, Ap
39	678	36.6	1766	10	US-09-809-391-254	Sequence 254, App
40	678	36.6	1766	10	US-09-882-171-254	Sequence 254, App
41	678	36.6	1766	17	US-10-164-861-254	Sequence 254, App
42	677	36.6	1915	17	US-10-276-774-980	Sequence 980, App
43	674	36.4	1668	9	US-09-765-205-25	Sequence 25, Appl
44	674	36.4	2768	18	US-10-723-860-6867	Sequence 6867, Ap
45	672	36.3	422	9	US-09-960-352-11567	Sequence 11567, A

# ALIGNMENTS

## RESULT 1

US-09-789-386-5  
; Sequence 5, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1122  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-5

## Alignment Scores:

Pred. No.:	5.13e-152	Length:	1122
Score:	1829.00	Matches:	360
Percent Similarity:	96.51%	Conservative:	0
Best Local Similarity:	96.51%	Mismatches:	1
Query Match:	98.86%	Indels:	12
DB:	9	Gaps:	1

SEQ29 (1-361) x US-09-789-386-5 (1-1122)

Qy	1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln	20
Db	1 ATGGAAGACCTGGACCACTCTCCTCTGGTCTCGTCTCGGACAGCCACCCCGGCCGAG	60
Qy	21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGlu	40
Db	61 CCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAGGAAGAAGAGGAGGAG	120

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 14, 2005, 17:27:17 ; Search time 4007.05 Seconds  
(without alignments)  
3429.256 Million cell updates/sec

Title: SEQ29  
Perfect score: 1850  
Sequence: 1 MEDLDQSPVLVSSSDSPFRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/NICHOLS-09-830-672-  
FUSION/runat\_14042005\_104546\_4021/app\_query.fasta\_1.1038  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=NICHOLS-09-830-672-FUSION @CGN 1 1 5533 @runat\_14042005\_104546\_4021  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query					Description
	No.	Score	Match Length	DB	ID	
	1	1485.5	80.3	3533	3	AK034902 Mus muscu
	2	1246	67.4	1097	5	BX439214 BX439214
	3	1167	63.1	911	1	AL549191 AL549191
	4	1080.5	58.4	781	4	BI079496 602876306
	5	1030.5	55.7	1002	5	BX462171 BX462171
	6	978	52.9	677	7	CN791158 4125836 B
	7	954.5	51.6	924	5	BU845601 AGENCOURT
	8	939	50.8	667	7	CN429712 170006000
	9	932.5	50.4	708	4	BI157842 602923001
	10	927	50.1	598	7	CF118424 fs543.z1
	11	927	50.1	600	9	AY404970 Homo sapi
	12	927	50.1	650	6	CB215381 NISC_np05
	13	927	50.1	672	7	CK977984 4109431 B
	14	927	50.1	682	6	CB162885 K-EST0223
	15	927	50.1	712	7	CK971318 4087182 B
	16	927	50.1	743	6	CD102817 AGENCOURT
	17	927	50.1	758	4	BG697436 602660623
	18	927	50.1	788	1	AL533461 AL533461
	19	927	50.1	843	4	BG570231 602590632
	20	927	50.1	849	7	CR765672 DKFZp469C
c	21	927	50.1	875	1	AL573494 AL573494
	22	927	50.1	1540	3	CR611869 full-leng
	23	927	50.1	1785	3	AF077050 Homo sapi
	24	924	49.9	730	1	AU297347 AU297347
	25	923.5	49.9	810	4	BI080232 602876650
	26	923	49.9	592	7	CN482802 hw24h12.y
	27	921	49.8	634	6	CB067821 iq38a06.y
	28	921	49.8	670	7	CV030029 9024 Full
	29	921	49.8	960	7	CN646472 ILLUMIGEN
	30	921	49.8	983	7	CN803408 ILLUMIGEN
	31	921	49.8	1031	7	CN647521 ILLUMIGEN
	32	915	49.5	805	7	CO735185 S1LE04c10
	33	915	49.5	958	4	BM801698 AGENCOURT
	34	914	49.4	679	4	BI149602 602848410
	35	914	49.4	757	4	BG715173 602675631
	36	913	49.4	779	7	CO401465 AGENCOURT
	37	913	49.4	1042	7	CN805577 ILLUMIGEN
	38	912	49.3	871	6	CD110203 AGENCOURT
	39	911	49.2	600	9	AY404972 Mus muscu
	40	908	49.1	1013	7	CO048918 ILLUMIGEN
	41	908	49.1	1018	7	CN801888 ILLUMIGEN
	42	906	49.0	990	4	BI691132 603314519
	43	905	48.9	794	1	AU080127 AU080127
	44	905	48.9	799	1	AU080133 AU080133
	45	904	48.9	695	7	CV077130 AGENCOURT

# ALIGNMENTS

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:35:57 ; Search time 82.5388 Seconds  
(without alignments)  
3746.799 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094844\_18372/app\_query.fasta\_1  
.3683

-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_@CGN\_1\_1\_255\_@runat\_14042005\_094844\_18372 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%				DB	ID	Description
	No.	Score	Query Match	Length			
	1	931	100.0	4822	3	US-09-484-970B-106	Sequence 106, App
	2	927	99.6	799	2	US-08-700-607-2	Sequence 2, Appli
	3	927	99.6	1669	4	US-09-949-016-3253	Sequence 3253, Ap
	4	914	98.2	2610	4	US-09-023-655-382	Sequence 382, App
	5	682	73.3	2069	4	US-09-949-016-3309	Sequence 3309, Ap
	6	682	73.3	3202	4	US-09-949-016-1127	Sequence 1127, Ap
	7	627.5	67.4	2262	4	US-09-949-016-2988	Sequence 2988, Ap
	8	624.5	67.1	1766	3	US-09-149-476-254	Sequence 254, App
	9	624.5	67.1	2664	3	US-09-149-476-255	Sequence 255, App
	10	543	58.3	3517	4	US-09-799-451-111	Sequence 111, App
	11	526.5	56.6	1095	2	US-08-700-607-4	Sequence 4, Appli
	12	518	55.6	2014	4	US-09-270-767-13561	Sequence 13561, A
	13	508.5	54.6	794	3	US-09-149-476-102	Sequence 102, App
	14	473.5	50.9	2181	4	US-09-949-016-1419	Sequence 1419, Ap
c	15	341	36.6	601	4	US-09-949-016-117588	Sequence 117588,
c	16	341	36.6	601	4	US-09-949-016-117589	Sequence 117589,
	17	341	36.6	42075	4	US-09-949-016-14995	Sequence 14995, A
	18	286	30.7	443	4	US-09-513-999C-3784	Sequence 3784, Ap
	19	279.5	30.0	135667	4	US-09-949-016-15051	Sequence 15051, A
	20	279.5	30.0	152486	4	US-09-949-016-12869	Sequence 12869, A
c	21	276.5	29.7	601	4	US-09-949-016-40169	Sequence 40169, A
c	22	276.5	29.7	601	4	US-09-949-016-119335	Sequence 119335,
	23	276	29.6	261	2	US-08-700-607-9	Sequence 9, Appli
	24	271	29.1	13906	4	US-09-949-016-14730	Sequence 14730, A
	25	256	27.5	200	4	US-09-513-999C-11198	Sequence 11198, A
	26	236.5	25.4	15661	4	US-09-949-016-13161	Sequence 13161, A
	27	144	15.5	1125	4	US-09-248-796A-1905	Sequence 1905, Ap
c	28	141	15.1	601	4	US-09-949-016-40170	Sequence 40170, A
c	29	141	15.1	601	4	US-09-949-016-119336	Sequence 119336,
c	30	122	13.1	601	4	US-09-949-016-117609	Sequence 117609,
	31	111	11.9	266	4	US-09-313-294A-703	Sequence 703, App
c	32	102	11.0	601	4	US-09-949-016-48087	Sequence 48087, A
	33	100	10.7	425	3	US-08-905-223-178	Sequence 178, App
c	34	95	10.2	1722	4	US-08-956-171E-407	Sequence 407, App
c	35	95	10.2	1722	4	US-08-781-986A-407	Sequence 407, App
	36	89	9.6	1828	3	US-08-487-596-7	Sequence 7, Appli
	37	89	9.6	1828	4	US-08-660-451A-7	Sequence 7, Appli
	38	88.5	9.5	4550	3	US-09-462-136-1	Sequence 1, Appli
	39	88.5	9.5	4661	4	US-09-949-016-4281	Sequence 4281, Ap
	40	88.5	9.5	4673	4	US-09-814-915A-100	Sequence 100, App
	41	88	9.5	1273	4	US-09-949-016-5725	Sequence 5725, Ap
	42	87.5	9.4	1779	4	US-09-134-000C-2072	Sequence 2072, Ap
	43	87.5	9.4	3156	3	US-09-134-001C-2168	Sequence 2168, Ap
	44	86	9.2	296	4	US-09-313-294A-81	Sequence 81, Appl
	45	85	9.1	1302	4	US-08-956-171E-322	Sequence 322, App

## ALIGNMENTS

RESULT 1

US-09-484-970B-106



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 22:42:49 ; Search time 290.373 Seconds  
(without alignments)  
3948.747 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094847\_18466/app\_query.fasta\_1  
.3683

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	931	100.0	3579	9	US-09-789-386-1	Sequence 1, Appli
2	931	100.0	3579	9	US-09-893-348-22	Sequence 22, Appl
3	931	100.0	3579	17	US-10-267-502-212	Sequence 212, App
4	931	100.0	3579	18	US-10-327-213-8	Sequence 8, Appli
5	931	100.0	3579	18	US-10-466-258-8	Sequence 8, Appli
6	931	100.0	3579	18	US-10-810-653-22	Sequence 22, Appl
7	931	100.0	4053	9	US-09-758-140-5	Sequence 5, Appli
8	931	100.0	4053	9	US-09-972-599A-5	Sequence 5, Appli
9	931	100.0	4053	18	US-10-717-597-310	Sequence 310, App
10	931	100.0	4632	14	US-10-060-036-53	Sequence 53, Appl
11	927	99.6	799	17	US-10-660-946-2	Sequence 2, Appli
12	927	99.6	1122	9	US-09-789-386-5	Sequence 5, Appli
13	927	99.6	1160	14	US-10-175-523-156	Sequence 156, App
14	927	99.6	1610	9	US-09-765-205-5	Sequence 5, Appli
15	927	99.6	1785	17	US-10-439-388-62	Sequence 62, Appl
16	927	99.6	2052	18	US-10-466-258-3	Sequence 3, Appli
17	927	99.6	2235	14	US-10-060-036-54	Sequence 54, Appl
18	921	98.9	1980	17	US-10-220-891-22	Sequence 22, Appl
19	918	98.6	994	11	US-09-978-360A-110	Sequence 110, App
20	914	98.2	2610	17	US-10-641-643-382	Sequence 382, App
21	908	97.5	4684	9	US-09-893-348-17	Sequence 17, Appl
22	908	97.5	4684	18	US-10-810-653-17	Sequence 17, Appl
23	905	97.2	2782	15	US-10-205-194-165	Sequence 165, App
24	904.5	97.2	3492	17	US-10-267-502-214	Sequence 214, App
25	886	95.2	1798	18	US-10-466-258-10	Sequence 10, Appl
26	867	93.1	1514	9	US-09-823-245A-349	Sequence 349, App
27	695	74.7	422	9	US-09-960-352-8477	Sequence 8477, Ap
28	682	73.3	1520	15	US-10-084-817-333	Sequence 333, App
29	682	73.3	2331	17	US-10-267-502-213	Sequence 213, App
30	682	73.3	3202	9	US-09-954-456-210	Sequence 210, App
31	682	73.3	3202	17	US-10-172-118-386	Sequence 386, App
32	682	73.3	3202	17	US-10-342-887-386	Sequence 386, App
33	682	73.3	3202	18	US-10-723-860-1480	Sequence 1480, Ap
34	682	73.3	3202	19	US-10-843-641A-3237	Sequence 3237, Ap
35	682	73.3	3305	18	US-10-723-860-5926	Sequence 5926, Ap

36	681	73.1	1502	15	US-10-205-219-94	Sequence 94, Appl
37	681	73.1	2343	17	US-10-267-502-215	Sequence 215, App
38	672	72.2	422	9	US-09-960-352-11567	Sequence 11567, A
39	665	71.4	1473	15	US-10-205-194-128	Sequence 128, App
40	624.5	67.1	711	17	US-10-408-967-1	Sequence 1, Appli
41	624.5	67.1	1330	15	US-10-106-698-1945	Sequence 1945, Ap
42	624.5	67.1	1656	9	US-09-729-674-19	Sequence 19, Appl
43	624.5	67.1	1656	18	US-10-913-553-19	Sequence 19, Appl
44	624.5	67.1	1668	9	US-09-765-205-25	Sequence 25, Appl
45	624.5	67.1	1766	10	US-09-809-391-254	Sequence 254, App

# ALIGNMENTS

## RESULT 1

US-09-789-386-1

```
; Sequence 1, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-1
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## Alignment Scores:

Pred. No.:	4.02e-106	Length:	3579
Score:	931.00	Matches:	189
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-789-386-1 (1-3579)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	3010	TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC	3069
Qy	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	3070	AGCCTATTCTGCTGCTTTTCATTGACAGTATTGAGCATTGTGAGCGTAACAGCCTACATT	3129

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:34:27 ; Search time 1670.87 Seconds  
(without alignments)  
4305.640 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094843\_18360/app\_query.fasta\_1  
.3683

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
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-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_@CGN\_1\_1\_13747\_@runat\_14042005\_094843\_18360 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
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3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	927	99.6	598	7	CF118424	CF118424 fs543.z1
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3	927	99.6	650	6	CB215381	CB215381 NISC_np05
4	927	99.6	667	7	CN429712	CN429712 170006000
5	927	99.6	672	7	CK977984	CK977984 4109431 B
6	927	99.6	682	6	CB162885	CB162885 K-EST0223
7	927	99.6	712	7	CK971318	CK971318 4087182 B
8	927	99.6	743	6	CD102817	CD102817 AGENCOURT
9	927	99.6	758	4	BG697436	BG697436 602660623
10	927	99.6	788	1	AL533461	AL533461 AL533461
11	927	99.6	843	4	BG570231	BG570231 602590632
12	927	99.6	849	7	CR765672	CR765672 DKF2p469C
c 13	927	99.6	875	1	AL573494	AL573494 AL573494
14	927	99.6	1540	3	CR611869	CR611869 full-leng
15	927	99.6	1785	3	AF077050	AF077050 Homo sapi
16	924	99.2	730	1	AU297347	AU297347 AU297347
17	921	98.9	634	6	CB067821	CB067821 iq38a06.y
18	921	98.9	670	7	CV030029	CV030029 9024 Full
19	921	98.9	960	7	CN646472	CN646472 ILLUMIGEN
20	921	98.9	983	7	CN803408	CN803408 ILLUMIGEN
21	921	98.9	1031	7	CN647521	CN647521 ILLUMIGEN
22	915	98.3	805	7	CO735185	CO735185 S1LE04c10
23	915	98.3	958	4	BM801698	BM801698 AGENCOURT
24	914	98.2	757	4	BG715173	BG715173 602675631
25	913	98.1	924	5	BU845601	BU845601 AGENCOURT
26	913	98.1	1042	7	CN805577	CN805577 ILLUMIGEN
27	912	98.0	592	7	CN482802	CN482802 hw24h12.y
28	912	98.0	871	6	CD110203	CD110203 AGENCOURT
29	911	97.9	600	9	AY404972	AY404972 Mus muscu
30	911	97.9	679	4	BI149602	BI149602 602848410
31	911	97.9	708	4	BI157842	BI157842 602923001
32	908	97.5	779	7	CO401465	CO401465 AGENCOURT
33	908	97.5	1013	7	CO048918	CO048918 ILLUMIGEN
34	908	97.5	1018	7	CN801888	CN801888 ILLUMIGEN
35	905	97.2	794	1	AU080127	AU080127 AU080127
36	905	97.2	799	1	AU080133	AU080133 AU080133
37	904	97.1	695	7	CV077130	CV077130 AGENCOURT
38	904	97.1	758	4	BG740561	BG740561 602633075
39	904	97.1	791	7	CF977898	CF977898 F26A06_04
40	904	97.1	1081	7	CN641703	CN641703 ILLUMIGEN
41	902	96.9	747	4	BG623462	BG623462 602648520
42	900	96.7	585	7	CO259245	CO259245 4130644 B
43	899	96.6	742	4	BI838242	BI838242 603083162
44	896	96.2	3533	3	AK034902	AK034902 Mus muscu
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# ALIGNMENTS

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:30:21 ; Search time 2310.43 Seconds  
(without alignments)  
3963.787 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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.3683

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_@CGN\_1\_1\_19954\_@runat\_14042005\_094842\_18348 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
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2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	931	100.0	2481	9	AF063601	AF063601 Homo sapi
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3	931	100.0	3491	9	AF333336	AF333336 Homo sapi
4	931	100.0	3576	6	AX766050	AX766050 Sequence
5	931	100.0	3579	6	BD249446	BD249446 Protein s
6	931	100.0	3579	9	HSA251383	AJ251383 Homo sapi
7	931	100.0	3919	6	CQ829486	CQ829486 Sequence
8	931	100.0	4053	6	AX195249	AX195249 Sequence
9	931	100.0	4053	9	AB020693	AB020693 Homo sapi
10	931	100.0	4060	9	AY123250	AY123250 Homo sapi
11	931	100.0	4070	9	AY123249	AY123249 Homo sapi
12	931	100.0	4093	6	BD270070	BD270070 Secreted
13	931	100.0	4102	9	AY123245	AY123245 Homo sapi
14	931	100.0	4109	9	AY123248	AY123248 Homo sapi
15	931	100.0	4123	9	AY123247	AY123247 Homo sapi
16	931	100.0	4160	9	AY123246	AY123246 Homo sapi
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19	931	100.0	4789	6	CQ874017	CQ874017 Sequence
20	931	100.0	4789	9	AY102279	AY102279 Homo sapi
21	931	100.0	4822	6	AR220865	AR220865 Sequence
22	928	99.7	1784	9	BC016165	BC016165 Homo sapi
23	928	99.7	2389	9	AY102278	AY102278 Homo sapi
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27	927	99.6	1122	6	BD249448	BD249448 Protein s
28	927	99.6	1122	9	HSA251384	AJ251384 Homo sapi
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30	927	99.6	1213	6	BD194907	BD194907 86 human
31	927	99.6	1213	6	CQ855235	CQ855235 Sequence
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33	927	99.6	1485	9	BC010737	BC010737 Homo sapi
34	927	99.6	1525	9	AK130812	AK130812 Homo sapi
35	927	99.6	1599	6	CQ769577	CQ769577 Sequence
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37	927	99.6	1617	9	AF087901	AF087901 Homo sapi
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39	927	99.6	1654	9	BC012619	BC012619 Homo sapi
40	927	99.6	1668	9	BC026788	BC026788 Homo sapi
41	927	99.6	1691	9	AF132048	AF132048 Homo sapi
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# ALIGNMENTS

## RESULT 1

AF063601

LOCUS AF063601 2481 bp mRNA linear PRI 02-JAN-2001

DEFINITION Homo sapiens brain my043 protein mRNA, complete cds.

ACCESSION AF063601

VERSION AF063601.1 GI:12002033

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2481)

AUTHORS Mao,Y.M., Xie,Y. and Zheng,Z.H.

TITLE Direct Submission

JOURNAL Submitted (05-MAY-1998) Institute of Genetics, School of Life Science, Fudan University, 220 Handan Rd., Shanghai 200433, P.R.China

## FEATURES

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CDS 194. .2137

/codon\_start=1

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KLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDFSDDSIPDVPQKQDET  
VMLVKESLTETSFSMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVST  
LSKKEKIPLQMEELSTAVYSNDDLFIKEAQIRETETFSDDSPIEIIDEFPTLISSKT  
DSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDD  
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FSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS  
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VDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG  
LA  
NKNVKDAMAKIQAKIPGLKRKAE"

## ORIGIN

### Alignment Scores:

Pred. No.:	5.99e-87	Length:	2481
Score:	931.00	Matches:	189
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:29:46 ; Search time 267.442 Seconds  
(without alignments)  
4183.459 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094842\_18342/app\_query.fasta\_1  
.3683

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-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_@CGN\_1\_1\_1955\_@runat\_14042005\_094842\_18342 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*

11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	931	100.0		3579	3	AAZ56886	Aaz56886 Human MAG
2	931	100.0		3579	4	AAF90324	Aaf90324 Human NOG
3	931	100.0		3579	6	ABK90134	Abk90134 DNA encod
4	931	100.0		3579	6	ABN86601	Abn86601 Human neu
5	931	100.0		3579	12	ADO07886	Ado07886 Human pol
6	931	100.0		3579	12	ADR13965	Adr13965 Human NOG
7	931	100.0		3833	3	AAD01174	Aad01174 Bovine ne
8	931	100.0		3919	12	ADP45550	Adp45550 Human Nog
9	931	100.0		4053	4	AAS09453	Aas09453 Human cDN
10	931	100.0		4053	9	ACC81048	Acc81048 Human Nog
11	931	100.0		4053	12	ADP13574	Adp13574 Renal cel
12	931	100.0		4093	3	AAA23454	Aaa23454 cDNA enco
13	931	100.0		4632	6	ABV94680	Abv94680 Human pan
14	931	100.0		4632	10	ADG32772	Adg32772 Human DNA
15	931	100.0		4698	8	ABX34563	Abx34563 Human mdd
16	931	100.0		4789	13	ADR83534	Adr83534 Human ret
17	931	100.0		4822	6	ABS70449	Abs70449 Human bon
c 18	928	99.7		1758	4	AAF32725	Aaf32725 Human sec
19	927	99.6		600	4	AAF90323	Aaf90323 Human NOG
20	927	99.6		770	3	AAA72983	Aaa72983 Human NSP
21	927	99.6		799	2	AAV23695	Aav23695 Human NSP
22	927	99.6		1122	3	AAZ56888	Aaz56888 Human MAG
23	927	99.6		1122	4	AAF90325	Aaf90325 Human NOG
24	927	99.6		1213	2	AAX04379	Aax04379 Human sec
25	927	99.6		1216	6	ABA05903	Aba05903 Human RTN
26	927	99.6		1599	10	ADI62860	Adi62860 Human apo
27	927	99.6		1610	3	AAZ36230	Aaz36230 cDNA enco
28	927	99.6		1785	12	ADK14166	Adk14166 Human aut
29	927	99.6		2052	6	ABK90133	Abk90133 DNA encod
30	927	99.6		2235	6	ABV94681	Abv94681 Human pan
31	927	99.6		2240	3	AAC64406	Aac64406 Human Nog
32	923	99.1		1694	4	AAK94408	Aak94408 Human ful
33	923	99.1		1694	12	ADL31137	Adl31137 Full leng
34	921	98.9		1980	4	AAI98079	Aai98079 Human neu
35	918	98.6		991	2	AAX97587	Aax97587 Extended
36	918	98.6		994	12	ADP18854	Adp18854 Human sec
37	914	98.2		2610	11	ADI31056	Adi31056 Human cDN
38	911	97.9		734	12	ADF42781	Adf42781 Mouse CYP
39	908	97.5		3492	12	ADP45571	Adp45571 Rat NogoA
40	908	97.5		4684	3	AAD01173	Aad01173 Rat neuro
41	908	97.5		4684	6	ABN86600	Abn86600 Rat neuro
42	905	97.2		2782	10	ADB85284	Adb85284 Rat fooce
43	904.5	97.2		3492	12	ADO07888	Ado07888 Mouse pol
44	904	97.1		1568	3	AAD01175	Aad01175 Rat neuro

## ALIGNMENTS

## RESULT 1

AAZ56886

ID AAZ56886 standard; DNA; 3579 BP.

XX

AC AAZ56886;

XX

DT 25-APR-2000 (first entry)

XX

DE Human MAGI polypeptide encoding DNA.

XX

KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
KW psychiatric disorder; developmental disorder; inflammatory disorder;  
KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .3579

FT /\*tag= a

FT /product= "MAGI polypeptide"

XX

PN WO200005364-A1.

XX

PD 03-FEB-2000.

XX

PF 21-JUL-1999; 99WO-GB002360.

XX

PR 22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.

XX

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha RK;

XX

DR WPI; 2000-182693/16.

DR P-PSDB; AAY56967.

XX

PT Novel polypeptides related to neuroendocrine-specific proteins and  
PT polynucleotides useful for diagnosis of various diseases and for  
PT treatment of cancer and neurological disorders.

XX

PS Claim 5; Page 19-20; 35pp; English.

XX

CC The invention relates to human MAGI protein, which is similar to  
CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
CC and antibodies are useful for treating diseases, including neuropathies,  
CC spinal injury, neuronal degeneration, neuromuscular disorders,  
CC psychiatric disorders and developmental disorders, cancer, stroke and  
CC inflammatory disorders. The polynucleotide is also useful for chromosome  
CC localization and for tissue expression studies. The present sequence

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:34:27 ; Search time 10414.2 Seconds  
(without alignments)  
4305.640 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094843\_18360/app\_query.fasta\_1  
.3683

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_CGN\_1\_1\_13747\_runat\_14042005\_094843\_18360 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
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2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

# SUMMARIES

Result	No.		Query		Match Length DB		ID	Description
			Score	Match	Length	DB		
	1	1339.5	22.6	1024	7	CN643847	CN643847	ILLUMIGEN
	2	1337.5	22.6	871	5	BQ719894	BQ719894	AGENCOURT
	3	1337	22.6	1013	7	CN646105	CN646105	ILLUMIGEN
	4	1314	22.2	898	7	CN641948	CN641948	ILLUMIGEN
	5	1304	22.0	901	7	CN646421	CN646421	ILLUMIGEN
	6	1291.5	21.8	954	4	BM470283	BM470283	AGENCOURT
	7	1279	21.6	902	7	CN805514	CN805514	ILLUMIGEN
	8	1224	20.7	1028	4	BM469346	BM469346	AGENCOURT
	9	1215	20.5	746	7	CR745036	CR745036	CR745036
	10	1202.5	20.3	969	4	BG706140	BG706140	602669409
	11	1183.5	20.0	730	4	BI601346	BI601346	603245090
	12	1153	19.5	699	4	BG819566	BG819566	602783209
	13	1135	19.2	3533	3	AK034902	AK034902	Mus muscu
	14	1122.5	19.0	896	6	CB204418	CB204418	AGENCOURT
	15	1092	18.4	671	7	CR751085	CR751085	DKFZp459K
	16	1091	18.4	842	5	BU709149	BU709149	UI-M-EW0-
c	17	1090	18.4	836	5	BX434904	BX434904	BX434904
	18	1087.5	18.4	863	2	BE783092	BE783092	601470682
	19	1087	18.4	986	5	BU841009	BU841009	AGENCOURT
	20	1067	18.0	742	7	CR751121	CR751121	DKFZp459L
	21	1064.5	18.0	695	7	CR749940	CR749940	DKFZp459C
	22	1063	17.9	822	6	CB521332	CB521332	UI-M-GH0-
	23	1032	17.4	785	6	CA511870	CA511870	UI-R-FJ0-
	24	1016.5	17.2	778	5	BU709106	BU709106	UI-M-EW0-
c	25	1015	17.1	619	1	AI879953	AI879953	au49b09.x
	26	1011.5	17.1	803	7	CN539361	CN539361	UI-M-HU0-
	27	998.5	16.9	805	4	BI730192	BI730192	603349739
c	28	997	16.8	611	4	BM669752	BM669752	UI-E-DX1-
	29	994.5	16.8	626	5	BQ639205	BQ639205	hd32f03.y
	30	976	16.5	779	7	CO401465	CO401465	AGENCOURT
	31	971	16.4	969	5	BU839934	BU839934	AGENCOURT
	32	965	16.3	580	5	BP255731	BP255731	BP255731
	33	962	16.2	582	5	BP229805	BP229805	BP229805
	34	961	16.2	613	7	CR630625	CR630625	DKFZp459B
	35	960.5	16.2	632	2	BE254391	BE254391	601109150
	36	956.5	16.1	714	7	CN532333	CN532333	UI-M-HQ0-
	37	955	16.1	582	5	BP219890	BP219890	BP219890
	38	955	16.1	1028	5	BU139629	BU139629	603134795
	39	954	16.1	584	5	BP220494	BP220494	BP220494
	40	954	16.1	592	5	BP307780	BP307780	BP307780
	41	952.5	16.1	573	5	BP208477	BP208477	BP208477
	42	951	16.1	589	1	AL705563	AL705563	DKFZp686I
	43	949.5	16.0	772	7	CF948588	CF948588	UI-M-HJ0-
	44	949	16.0	592	7	CN429731	CN429731	170004245
	45	948	16.0	582	5	BP310483	BP310483	BP310483

# ALIGNMENTS

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:30:21 ; Search time 2310.43 Seconds  
(without alignments)  
3963.787 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWWDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRRKAD 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094842\_18348/app\_query.fasta\_1  
.3683

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	925	100.0	3489	6	AX766046	AX766046 Sequence
2	925	100.0	3492	6	CQ829507	CQ829507 Sequence
3	925	100.0	4684	10	RNO242961	AJ242961 Rattus no
4	922	99.7	2782	6	AX700396	AX700396 Sequence
5	922	99.7	2782	10	AY164741	AY164741 Rattus no
6	922	99.7	2782	10	AF132045	AF132045 Rattus no
7	921	99.6	764	10	AF051335	AF051335 Rattus no
8	921	99.6	1568	10	RNO242963	AJ242963 Rattus no
9	921	99.6	2156	10	AY164740	AY164740 Rattus no
10	921	99.6	2156	10	RNO242962	AJ242962 Rattus no
11	921	99.6	2410	10	BC070879	BC070879 Rattus no
12	917	99.1	1738	10	AB073672	AB073672 Mus muscu
13	917	99.1	2958	10	BC032192	BC032192 Mus muscu
14	917	99.1	3815	10	BC032272	BC032272 Mus muscu
15	917	99.1	4063	10	AY102280	AY102280 Mus muscu
16	917	99.1	4518	10	BC056373	BC056373 Mus muscu
17	917	99.1	4627	10	AY102284	AY102284 Mus muscu
18	914	98.8	2266	10	AY102282	AY102282 Mus muscu
19	913	98.7	734	10	AF326337	AF326337 Mus muscu
20	913	98.7	1769	10	AY102283	AY102283 Mus muscu
21	913	98.7	2209	10	AY102281	AY102281 Mus muscu
22	908	98.2	2481	9	AF063601	AF063601 Homo sapi
23	908	98.2	2883	9	AF320999	AF320999 Homo sapi
24	908	98.2	3491	9	AF333336	AF333336 Homo sapi
25	908	98.2	3576	6	AX766050	AX766050 Sequence
26	908	98.2	3579	6	BD249446	BD249446 Protein s
27	908	98.2	3579	9	HSA251383	AJ251383 Homo sapi
28	908	98.2	3919	6	CQ829486	CQ829486 Sequence
29	908	98.2	4053	6	AX195249	AX195249 Sequence
30	908	98.2	4053	9	AB020693	AB020693 Homo sapi
31	908	98.2	4060	9	AY123250	AY123250 Homo sapi
32	908	98.2	4070	9	AY123249	AY123249 Homo sapi
33	908	98.2	4093	6	BD270070	BD270070 Secreted
34	908	98.2	4102	9	AY123245	AY123245 Homo sapi
35	908	98.2	4109	9	AY123248	AY123248 Homo sapi
36	908	98.2	4123	9	AY123247	AY123247 Homo sapi
37	908	98.2	4160	9	AY123246	AY123246 Homo sapi
38	908	98.2	4166	9	AB040462	AB040462 Homo sapi
39	908	98.2	4632	9	AF148537	AF148537 Homo sapi
40	908	98.2	4789	6	CQ874017	CQ874017 Sequence
41	908	98.2	4789	9	AY102279	AY102279 Homo sapi
42	908	98.2	4822	6	AR220865	AR220865 Sequence
43	906.5	98.0	3821	10	AY114152	AY114152 Mus muscu

44	905	97.8	1784	9	BC016165	BC016165 Homo sapi
45	905	97.8	2389	9	AY102278	AY102278 Homo sapi

# ALIGNMENTS

## RESULT 1

AX766046

LOCUS AX766046 3489 bp DNA linear PAT 25-JUN-2003

DEFINITION Sequence 1 from Patent WO03002602.

ACCESSION AX766046

VERSION AX766046.1 GI:32260128

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1

AUTHORS Eisenbach-Schwartz,M. and Hauben,E.

TITLE Nogo and nogo receptor derived peptides for t-cell mediated  
neuroprotection

JOURNAL Patent: WO 03002602-A 1 09-JAN-2003;  
YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)

FEATURES Location/Qualifiers

source 1. .3489  
/organism="Rattus norvegicus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10116"  
exon 1. .3489

ORIGIN

## Alignment Scores:

Pred. No.:	2.82e-85	Length:	3489
Score:	925.00	Matches:	189
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AX766046 (1-3489)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	2923	TCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCC	2982
Qy	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	2983	AGCTTATTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTTGTCAGTGTACGGCCTACATT	3042
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	3043	GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCT	3102
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	3103	ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATA	3162



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:29:46 ; Search time 267.442 Seconds  
(without alignments)  
4183.459 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRRKAD 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094842\_18342/app\_query.fasta\_1  
.3683

-DB=N\_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_@CGN\_1\_1\_1955\_@runat\_14042005\_094842\_18342 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:\*\n1: geneseqn1980s:\*\n2: geneseqn1990s:\*\n3: geneseqn2000s:\*\n4: geneseqn2001as:\*\n5: geneseqn2001bs:\*\n6: geneseqn2002as:\*\n7: geneseqn2002bs:\*\n8: geneseqn2003as:\*\n9: geneseqn2003bs:\*\n10: geneseqn2003cs:\*

11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
	1	925	100.0	3492	12	ADP45571	Adp45571 Rat NogoA
	2	925	100.0	4684	3	AAD01173	Aad01173 Rat neuro
	3	925	100.0	4684	6	ABN86600	Abn86600 Rat neuro
	4	922	99.7	2782	10	ADB85284	Adb85284 Rat fooce
	5	921	99.6	1568	3	AAD01175	Aad01175 Rat neuro
	6	913	98.7	734	12	ADF42781	Adf42781 Mouse CYP
	7	908	98.2	3579	3	AAZ56886	Aaz56886 Human MAG
	8	908	98.2	3579	4	AAF90324	Aaf90324 Human NOG
	9	908	98.2	3579	6	ABK90134	Abk90134 DNA encod
	10	908	98.2	3579	6	ABN86601	Abn86601 Human neu
	11	908	98.2	3579	12	ADO07886	Ado07886 Human pol
	12	908	98.2	3579	12	ADR13965	Adr13965 Human NOG
	13	908	98.2	3833	3	AAD01174	Aad01174 Bovine ne
	14	908	98.2	3919	12	ADP45550	Adp45550 Human Nog
	15	908	98.2	4053	4	AAS09453	Aas09453 Human cDN
	16	908	98.2	4053	9	ACC81048	Acc81048 Human Nog
	17	908	98.2	4053	12	ADP13574	Adp13574 Renal cel
	18	908	98.2	4093	3	AAA23454	Aaa23454 cDNA enco
	19	908	98.2	4632	6	ABV94680	Abv94680 Human pan
	20	908	98.2	4632	10	ADG32772	Adg32772 Human DNA
	21	908	98.2	4698	8	ABX34563	Abx34563 Human mdd
	22	908	98.2	4789	13	ADR83534	Adr83534 Human ret
	23	908	98.2	4822	6	ABS70449	Abs70449 Human bon
	24	906.5	98.0	3492	12	ADO07888	Ado07888 Mouse pol
c	25	905	97.8	1758	4	AAF32725	Aaf32725 Human sec
	26	904	97.7	600	4	AAF90323	Aaf90323 Human NOG
	27	904	97.7	770	3	AAA72983	Aaa72983 Human NSP
	28	904	97.7	799	2	AAV23695	Aav23695 Human NSP
	29	904	97.7	1122	3	AAZ56888	Aaz56888 Human MAG
	30	904	97.7	1122	4	AAF90325	Aaf90325 Human NOG
	31	904	97.7	1213	2	AAX04379	Aax04379 Human sec
	32	904	97.7	1216	6	ABA05903	Aba05903 Human RTN
	33	904	97.7	1599	10	ADI62860	Adi62860 Human apo
	34	904	97.7	1610	3	AAZ36230	Aaz36230 cDNA enco
	35	904	97.7	1785	12	ADK14166	Adk14166 Human aut
	36	904	97.7	2052	6	ABK90133	Abk90133 DNA encod
	37	904	97.7	2235	6	ABV94681	Abv94681 Human pan
	38	904	97.7	2240	3	AAC64406	Aac64406 Human Nog
	39	900	97.3	1694	4	AAK94408	Aak94408 Human ful
	40	900	97.3	1694	12	ADL31137	Adl31137 Full leng
	41	898	97.1	1980	4	AAI98079	Aai98079 Human neu
	42	895	96.8	991	2	AAX97587	Aax97587 Extended
	43	895	96.8	994	12	ADP18854	Adp18854 Human sec
	44	891	96.3	2610	11	ADI31056	Adi31056 Human cDN

## ALIGNMENTS

## RESULT 1

ADP45571

ID ADP45571 standard; cDNA; 3492 BP.

XX

AC ADP45571;

XX

DT 09-SEP-2004 (first entry)

XX

DE Rat NogoA encoding cDNA SEQ ID NO:25.

XX

KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;

KW nerve repair; neuroprotective; gene therapy;

KW central nervous system injury; CNS injury; neurodegenerative disorder;

KW rat; gene; ss.

XX

OS Rattus norvegicus.

XX

FH Key Location/Qualifiers

FT CDS 1..3492

FT /\*tag= a

FT /product= "NogoA"

XX

PN WO2004052932-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-EP013960.

XX

PR 10-DEC-2002; 2002GB-00028832..

XX

PA (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS PHARMA GMBH.

PA (UYZU-) UNIV ZUERICH.

XX

PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

PI Zurini M;

XX

DR WPI; 2004-468818/44.

DR P-PSDB; ADP45572.

XX

PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-

PT D20 or NogoA623-640, useful in preparing a composition for treating CNS

PT injury or neurodegenerative disorders.

XX

PS Disclosure; SEQ ID NO 25; 121pp; English.

XX

CC The present invention describes a binding molecule which binds to human  
CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a  
CC dissociation constant of less than 1000nM. Also described: (1) a  
CC polynucleotide encoding the binding molecule; (2) an expression vector or  
CC system comprising the polynucleotide; (3) a host cell comprising the  
CC expression system; (4) a pharmaceutical composition comprising the

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:35:57 ; Search time 82.5388 Seconds  
(without alignments)  
3746.799 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094844\_18372/app\_query.fasta\_1  
.3683

-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_@CGN\_1\_1\_255\_@runat\_14042005\_094844\_18372 -NCPUs=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	8						Description
	No.	Score	Query Match	Length	DB	ID	
	1	908	98.2	4822	3	US-09-484-970B-106	Sequence 106, App
	2	904	97.7	799	2	US-08-700-607-2	Sequence 2, Appli
	3	904	97.7	1669	4	US-09-949-016-3253	Sequence 3253, Ap
	4	891	96.3	2610	4	US-09-023-655-382	Sequence 382, App
	5	679	73.4	2069	4	US-09-949-016-3309	Sequence 3309, Ap
	6	679	73.4	3202	4	US-09-949-016-1127	Sequence 1127, Ap
	7	625.5	67.6	2262	4	US-09-949-016-2988	Sequence 2988, Ap
	8	622.5	67.3	1766	3	US-09-149-476-254	Sequence 254, App
	9	622.5	67.3	2664	3	US-09-149-476-255	Sequence 255, App
	10	541	58.5	3517	4	US-09-799-451-111	Sequence 111, App
	11	524.5	56.7	1095	2	US-08-700-607-4	Sequence 4, Appli
	12	518	56.0	2014	4	US-09-270-767-13561	Sequence 13561, A
	13	509.5	55.1	794	3	US-09-149-476-102	Sequence 102, App
	14	475	51.4	2181	4	US-09-949-016-1419	Sequence 1419, Ap
c	15	341	36.9	601	4	US-09-949-016-117588	Sequence 117588,
c	16	341	36.9	601	4	US-09-949-016-117589	Sequence 117589,
	17	341	36.9	42075	4	US-09-949-016-14995	Sequence 14995, A
	18	286	30.9	443	4	US-09-513-999C-3784	Sequence 3784, Ap
	19	282.5	30.5	135667	4	US-09-949-016-15051	Sequence 15051, A
	20	282.5	30.5	152486	4	US-09-949-016-12869	Sequence 12869, A
c	21	278.5	30.1	601	4	US-09-949-016-40169	Sequence 40169, A
c	22	278.5	30.1	601	4	US-09-949-016-119335	Sequence 119335,
	23	276	29.8	261	2	US-08-700-607-9	Sequence 9, Appli
	24	271	29.3	13906	4	US-09-949-016-14730	Sequence 14730, A
	25	248	26.8	15661	4	US-09-949-016-13161	Sequence 13161, A
	26	243	26.3	200	4	US-09-513-999C-11198	Sequence 11198, A
c	27	146	15.8	601	4	US-09-949-016-40170	Sequence 40170, A
c	28	146	15.8	601	4	US-09-949-016-119336	Sequence 119336,
	29	142	15.4	1125	4	US-09-248-796A-1905	Sequence 1905, Ap
c	30	114	12.3	601	4	US-09-949-016-117609	Sequence 117609,
	31	109	11.8	266	4	US-09-313-294A-703	Sequence 703, App
c	32	102	11.0	601	4	US-09-949-016-48087	Sequence 48087, A
	33	100	10.8	425	3	US-08-905-223-178	Sequence 178, App
	34	95	10.3	1828	3	US-08-487-596-7	Sequence 7, Appli
	35	95	10.3	1828	4	US-08-660-451A-7	Sequence 7, Appli
	36	94	10.2	1273	4	US-09-949-016-5725	Sequence 5725, Ap
c	37	94	10.2	1722	4	US-08-956-171E-407	Sequence 407, App
c	38	94	10.2	1722	4	US-08-781-986A-407	Sequence 407, App
	39	92.5	10.0	12566	3	US-08-961-527-149	Sequence 149, App
	40	88.5	9.6	4550	3	US-09-462-136-1	Sequence 1, Appli
	41	88.5	9.6	4661	4	US-09-949-016-4281	Sequence 4281, Ap
	42	88.5	9.6	4673	4	US-09-814-915A-100	Sequence 100, App
	43	86.5	9.4	296	4	US-09-313-294A-81	Sequence 81, Appl
	44	86.5	9.4	1779	4	US-09-134-000C-2072	Sequence 2072, Ap
	45	86	9.3	1302	4	US-08-956-171E-322	Sequence 322, App

## ALIGNMENTS

RESULT 1

US-09-484-970B-106

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:34:27 ; Search time 1670.87 Seconds  
(without alignments)  
4305.640 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWDRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlh

-  
Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094843\_18360/app\_query.fasta\_1  
.3683  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972\_CGN\_1\_1\_13747@runat\_14042005\_094843\_18360 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	925	100.0	779	7	CO401465	CO401465 AGENCOURT
2	921	99.6	695	7	CV077130	CV077130 AGENCOURT
3	921	99.6	791	7	CF977898	CF977898 F26A06_04
4	913	98.7	600	9	AY404972	AY404972 Mus muscu
5	913	98.7	679	4	BI149602	BI149602 602848410
6	913	98.7	708	4	BI157842	BI157842 602923001
7	907	98.1	794	1	AU080127	AU080127 AU080127
8	907	98.1	799	1	AU080133	AU080133 AU080133
9	904	97.7	598	7	CF118424	CF118424 fs543.z1
10	904	97.7	600	9	AY404970	AY404970 Homo sapi
11	904	97.7	650	6	CB215381	CB215381 NISC_np05
12	904	97.7	667	7	CN429712	CN429712 170006000
13	904	97.7	672	7	CK977984	CK977984 4109431 B
14	904	97.7	682	6	CB162885	CB162885 K-EST0223
15	904	97.7	712	7	CK971318	CK971318 4087182 B
16	904	97.7	743	6	CD102817	CD102817 AGENCOURT
17	904	97.7	758	4	BG697436	BG697436 602660623
18	904	97.7	788	1	AL533461	AL533461 AL533461
19	904	97.7	843	4	BG570231	BG570231 602590632
20	904	97.7	849	7	CR765672	CR765672 DKFZp469C
c 21	904	97.7	875	1	AL573494	AL573494 AL573494
22	904	97.7	1540	3	CR611869	CR611869 full-leng
23	904	97.7	1785	3	AF077050	AF077050 Homo sapi
24	903	97.6	781	4	BI079496	BI079496 602876306
25	901	97.4	730	1	AU297347	AU297347 AU297347
26	898	97.1	634	6	CB067821	CB067821 iq38a06.y
27	898	97.1	670	7	CV030029	CV030029 9024 Full
28	898	97.1	960	7	CN646472	CN646472 ILLUMIGEN
29	898	97.1	983	7	CN803408	CN803408 ILLUMIGEN
30	898	97.1	1031	7	CN647521	CN647521 ILLUMIGEN
31	898	97.1	3533	3	AK034902	AK034902 Mus muscu
32	895	96.8	990	4	BI691132	BI691132 603314519
33	894	96.6	751	7	CK357937	CK357937 AGENCOURT
34	893	96.5	718	1	AA986233	AA986233 uc73g12.y
35	892	96.4	592	7	CN482802	CN482802 hw24h12.y
36	892	96.4	805	7	CO735185	CO735185 S1LE04c10
37	892	96.4	958	4	BM801698	BM801698 AGENCOURT
38	891	96.3	749	4	BG296048	BG296048 602393712
39	891	96.3	757	4	BG715173	BG715173 602675631
40	890	96.2	924	5	BU845601	BU845601 AGENCOURT
41	890	96.2	1042	7	CN805577	CN805577 ILLUMIGEN
42	889	96.1	871	6	CD110203	CD110203 AGENCOURT
43	887	95.9	921	5	BU503291	BU503291 AGENCOURT
44	885	95.7	1013	7	CO048918	CO048918 ILLUMIGEN
45	885	95.7	1018	7	CN801888	CN801888 ILLUMIGEN

# ALIGNMENTS

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 22:42:49 ; Search time 290.373 Seconds  
(without alignments)  
3948.747 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09830972/runat\_14042005\_094847\_18466/app\_query.fasta\_1  
.3683  
-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09830972\_CGN\_1\_1\_2092@runat\_14042005\_094847\_18466  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	925	100.0	4684	9	US-09-893-348-17	Sequence 17, Appl
2	925	100.0	4684	18	US-10-810-653-17	Sequence 17, Appl
3	922	99.7	2782	15	US-10-205-194-165	Sequence 165, App
4	908	98.2	3579	9	US-09-789-386-1	Sequence 1, Appli
5	908	98.2	3579	9	US-09-893-348-22	Sequence 22, Appl
6	908	98.2	3579	17	US-10-267-502-212	Sequence 212, App
7	908	98.2	3579	18	US-10-327-213-8	Sequence 8, Appli
8	908	98.2	3579	18	US-10-466-258-8	Sequence 8, Appli
9	908	98.2	3579	18	US-10-810-653-22	Sequence 22, Appl
10	908	98.2	4053	9	US-09-758-140-5	Sequence 5, Appli
11	908	98.2	4053	9	US-09-972-599A-5	Sequence 5, Appli
12	908	98.2	4053	18	US-10-717-597-310	Sequence 310, App
13	908	98.2	4632	14	US-10-060-036-53	Sequence 53, Appl
14	906.5	98.0	3492	17	US-10-267-502-214	Sequence 214, App
15	904	97.7	799	17	US-10-660-946-2	Sequence 2, Appli
16	904	97.7	1122	9	US-09-789-386-5	Sequence 5, Appli
17	904	97.7	1160	14	US-10-175-523-156	Sequence 156, App
18	904	97.7	1610	9	US-09-765-205-5	Sequence 5, Appli
19	904	97.7	1785	17	US-10-439-388-62	Sequence 62, Appl
20	904	97.7	2052	18	US-10-466-258-3	Sequence 3, Appli
21	904	97.7	2235	14	US-10-060-036-54	Sequence 54, Appl
22	898	97.1	1980	17	US-10-220-891-22	Sequence 22, Appl
23	895	96.8	994	11	US-09-978-360A-110	Sequence 110, App
24	891	96.3	2610	17	US-10-641-643-382	Sequence 382, App
25	864	93.4	1798	18	US-10-466-258-10	Sequence 10, Appl
26	844	91.2	1514	9	US-09-823-245A-349	Sequence 349, App
27	679	73.4	1520	15	US-10-084-817-333	Sequence 333, App
28	679	73.4	2331	17	US-10-267-502-213	Sequence 213, App
29	679	73.4	3202	9	US-09-954-456-210	Sequence 210, App
30	679	73.4	3202	17	US-10-172-118-386	Sequence 386, App
31	679	73.4	3202	17	US-10-342-887-386	Sequence 386, App
32	679	73.4	3202	18	US-10-723-860-1480	Sequence 1480, Ap
33	679	73.4	3202	19	US-10-843-641A-3237	Sequence 3237, Ap
34	679	73.4	3305	18	US-10-723-860-5926	Sequence 5926, Ap
35	678	73.3	1502	15	US-10-205-219-94	Sequence 94, Appl

36	678	73.3	2343	17	US-10-267-502-215	Sequence 215, App
37	675	73.0	422	9	US-09-960-352-8477	Sequence 8477, Ap
38	665	71.9	1473	15	US-10-205-194-128	Sequence 128, App
39	657	71.0	422	9	US-09-960-352-11567	Sequence 11567, A
40	622.5	67.3	711	17	US-10-408-967-1	Sequence 1, Appli
41	622.5	67.3	1330	15	US-10-106-698-1945	Sequence 1945, Ap
42	622.5	67.3	1656	9	US-09-729-674-19	Sequence 19, Appl
43	622.5	67.3	1656	18	US-10-913-553-19	Sequence 19, Appl
44	622.5	67.3	1668	9	US-09-765-205-25	Sequence 25, Appl
45	622.5	67.3	1766	10	US-09-809-391-254	Sequence 254, App

# ALIGNMENTS

## RESULT 1

US-09-893-348-17

; Sequence 17, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 4684

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (253)..(3744)

; OTHER INFORMATION:

US-09-893-348-17

## Alignment Scores:

Pred. No.:	1.2e-101	Length:	4684
Score:	925.00	Matches:	189
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:29:46 ; Search time 1666.91 Seconds  
(without alignments)  
4183.459 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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7: geneseqn2002bs:\*  
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9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*

11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	5815	98.2	3919	12	ADP45550	Adp45550 Human Nog
2	5815	98.2	4053	4	AAS09453	Aas09453 Human cDN
3	5815	98.2	4053	9	ACC81048	Acc81048 Human Nog
4	5815	98.2	4053	12	ADP13574	Adp13574 Renal cel
5	5815	98.2	4632	6	ABV94680	Abv94680 Human pan
6	5815	98.2	4632	10	ADG32772	Adg32772 Human DNA
7	5815	98.2	4789	13	ADR83534	Adr83534 Human ret
8	5810	98.1	3579	3	AAZ56886	Aaz56886 Human MAG
9	5810	98.1	3579	4	AAF90324	Aaf90324 Human NOG
10	5810	98.1	3579	6	ABK90134	Abk90134 DNA encod
11	5810	98.1	3579	6	ABN86601	Abn86601 Human neu
12	5810	98.1	3579	12	ADO07886	Ado07886 Human pol
13	5810	98.1	3579	12	ADR13965	Adr13965 Human NOG
14	5788	97.7	4093	3	AAA23454	Aaa23454 cDNA enco
15	5780.5	97.6	4698	8	ABX34563	Abx34563 Human mdd
16	5748	97.0	4822	6	ABS70449	Abs70449 Human bon
17	4296.5	72.5	3492	12	ADP45571	Adp45571 Rat NogoA
18	4296.5	72.5	4684	3	AAD01173	Aad01173 Rat neuro
19	4296.5	72.5	4684	6	ABN86600	Abn86600 Rat neuro
20	4277.5	72.2	3492	12	ADO07888	Ado07888 Mouse pol
21	3798.5	64.1	3833	3	AAD01174	Aad01174 Bovine ne
22	3306.5	55.8	2386	2	AAV30920	Aav30920 Human sec
23	3297.5	55.7	2386	5	AAF98399	Aaf98399 Human cDN
24	2731	46.1	60615	13	ADT89536	Adt89536 Mus muscu
25	2593.5	43.8	2425	12	ADO26412	Ado26412 Rat trunc
26	2511.5	42.4	1980	4	AAI98079	Aai98079 Human neu
27	2425.5	41.0	2248	12	ADO26411	Ado26411 Rat trunc
28	2425.5	41.0	2278	12	ADO26413	Ado26413 Rat trunc
29	1495.5	25.2	1122	3	AAZ56888	Aaz56888 Human MAG
30	1495.5	25.2	1122	4	AAF90325	Aaf90325 Human NOG
31	1495.5	25.2	1216	6	ABA05903	Aba05903 Human RTN
32	1495.5	25.2	1610	3	AAZ36230	Aaz36230 cDNA enco
33	1495.5	25.2	2235	6	ABV94681	Abv94681 Human pan
34	1495.5	25.2	2240	3	AAC64406	Aac64406 Human Nog
35	1491.5	25.2	1599	10	ADI62860	Adi62860 Human apo
36	1487.5	25.1	2052	6	ABK90133	Abk90133 DNA encod
37	1478.5	25.0	1694	4	AAK94408	Aak94408 Human ful
38	1478.5	25.0	1694	12	ADL31137	Adl31137 Full leng
39	1437.5	24.3	2100	8	ABT42936	Abt42936 Human neu
40	1417	23.9	868	3	AAZ56887	Aaz56887 Human MAG
41	1340	22.6	1683	4	AAD08386	Aad08386 Human sec
42	1225.5	20.7	2782	10	ADB85284	Adb85284 Rat fooce
43	981	16.6	555	12	ADQ16423	Adq16423 Nucleotid
44	981	16.6	2934	12	ADQ16433	Adq16433 Construct

## ALIGNMENTS

## RESULT 1

ADP45550

ID ADP45550 standard; cDNA; 3919 BP.

XX

AC ADP45550;

XX

DT 09-SEP-2004 (first entry)

XX

DE Human NogoA encoding cDNA SEQ ID NO:4.

XX

KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;

KW nerve repair; neuroprotective; gene therapy;

KW central nervous system injury; CNS injury; neurodegenerative disorder;

KW gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .3579

FT /\*tag= a

FT /product= "NogoA"

XX

PN WO2004052932-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-EP013960.

XX

PR 10-DEC-2002; 2002GB-00028832.

XX

PA (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS PHARMA GMBH.

PA (UYZU-) UNIV ZUERICH.

XX

PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

PI Zurini M;

XX

DR WPI; 2004-468818/44.

DR P-PSDB; ADP45551.

XX

PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.

XX

PS Example 1; SEQ ID NO 4; 121pp; English.

XX

CC The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a dissociation constant of less than 1000nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 11:35:57 ; Search time 514.448 Seconds  
(without alignments)  
3746.799 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
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1	5748	97.0	4822	3	US-09-484-970B-106	Sequence 106, App
2	931	15.7	799	2	US-08-700-607-2	Sequence 2, Appli
3	931	15.7	1669	4	US-09-949-016-3253	Sequence 3253, Ap
4	918	15.5	2610	4	US-09-023-655-382	Sequence 382, App
5	800.5	13.5	3202	4	US-09-949-016-1127	Sequence 1127, Ap
6	750	12.7	3517	4	US-09-799-451-111	Sequence 111, App
7	727.5	12.3	2069	4	US-09-949-016-3309	Sequence 3309, Ap
8	707	11.9	428	4	US-09-513-999C-923	Sequence 923, App
9	635	10.7	1766	3	US-09-149-476-254	Sequence 254, App
10	635	10.7	2664	3	US-09-149-476-255	Sequence 255, App
11	627.5	10.6	2262	4	US-09-949-016-2988	Sequence 2988, Ap
12	576	9.7	382	4	US-09-513-999C-11526	Sequence 11526, A
13	527.5	8.9	1095	2	US-08-700-607-4	Sequence 4, Appli
14	526.5	8.9	2014	4	US-09-270-767-13561	Sequence 13561, A
15	517	8.7	794	3	US-09-149-476-102	Sequence 102, App
16	514	8.7	2181	4	US-09-949-016-1419	Sequence 1419, Ap
17	347	5.9	441	4	US-09-513-999C-2227	Sequence 2227, Ap
18	344.5	5.8	454	4	US-09-621-976-740	Sequence 740, App
19	344.5	5.8	463	4	US-09-621-976-741	Sequence 741, App
c 20	341	5.8	601	4	US-09-949-016-117588	Sequence 117588,
c 21	341	5.8	601	4	US-09-949-016-117589	Sequence 117589,
22	341	5.8	42075	4	US-09-949-016-14995	Sequence 14995, A
23	305	5.1	7571	4	US-09-949-016-4366	Sequence 4366, Ap
24	305	5.1	8146	4	US-09-976-594-725	Sequence 725, App
25	305	5.1	11917	4	US-09-566-921-32	Sequence 32, Appl
26	305	5.1	101300	4	US-09-949-016-16108	Sequence 16108, A
27	301	5.1	145287	4	US-09-949-016-13530	Sequence 13530, A
28	301	5.1	145287	4	US-09-949-016-13531	Sequence 13531, A
29	294	5.0	443	4	US-09-513-999C-3784	Sequence 3784, Ap
30	288	4.9	8560	4	US-09-949-016-1788	Sequence 1788, Ap
31	288	4.9	8560	4	US-09-949-016-1789	Sequence 1789, Ap
32	280	4.7	135667	4	US-09-949-016-15051	Sequence 15051, A
33	280	4.7	152486	4	US-09-949-016-12869	Sequence 12869, A
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c 35	277	4.7	601	4	US-09-949-016-119335	Sequence 119335,
36	276.5	4.7	5361	3	US-08-973-462-2	Sequence 2, Appli
37	276.5	4.7	6152	3	US-08-973-462-1	Sequence 1, Appli
38	276	4.7	261	2	US-08-700-607-9	Sequence 9, Appli
39	271	4.6	13906	4	US-09-949-016-14730	Sequence 14730, A
40	265	4.5	5200	4	US-08-978-277A-3	Sequence 3, Appli
41	264.5	4.5	8224	6	5180808-1	Patent No. 5180808
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43	261	4.4	14770	4	US-09-949-016-1107	Sequence 1107, Ap
44	258	4.4	13187	4	US-09-949-016-5062	Sequence 5062, Ap
45	257.5	4.3	6608	4	US-09-220-132-58	Sequence 58, Appl

## ALIGNMENTS

RESULT 1

US-09-484-970B-106

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 22:42:49 ; Search time 1809.84 Seconds  
(without alignments)  
3948.747 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPILVSSSDSPPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	5815	98.2	4053	18	US-10-717-597-310	Sequence 310, App
4	5815	98.2	4632	14	US-10-060-036-53	Sequence 53, Appl
5	5810	98.1	3579	9	US-09-789-386-1	Sequence 1, Appli
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## ALIGNMENTS

## RESULT 1

US-09-758-140-5

; Sequence 5, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth

; FILE REFERENCE: 44574-5073-US

; CURRENT APPLICATION NUMBER: US/09/758,140

; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: US 60/175,707

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: US 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,378

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 20

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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 5

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; ORGANISM: Homo sapiens

; FEATURE:

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; NAME/KEY: CDS
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; LOCATION: (135)..(3710)
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; OTHER INFORMATION: Human mRNA for No. US20020012965A1o protein (KIAA0886,  
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; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)

US-09-758-140-5

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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# ALIGNMENTS

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LOCUS CQ829486 3919 bp DNA linear PAT 05-JUL-2004

DEFINITION Sequence 4 from Patent WO2004052932.

ACCESSION CQ829486

VERSION CQ829486.1 GI:49732808

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Barske,C., Mir,A.K., Oertle,T., Schnell,L., Schwab,M.E.,  
Vitaliti,A. and Zurini,M.

TITLE Nogo a binding molecules and pharmaceutical use thereof

JOURNAL Patent: WO 2004052932-A 4 24-JUN-2004;

Novartis AG (CH)

FEATURES Location/Qualifiers

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Db	1261	GATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAACGAAAAAGATAGTGAGAGT	1320



Qy 427 SerAsnAspAspThrSerPheProSerThrProGluGlyIleLysAspArgSerGlyAla 446  
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 Db 1321 AGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGATCGTCCAGGAGCA 1380

Qy 447 TyrIleThrCysAlaProPheAsnProAlaAlaThrGluSerIleAlaThrAsnIlePhe 466  
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 Db 1381 TATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCAACAAACATTTTT 1440

Qy 467 ProLeuLeuGluAspProThrSerGluAsn\*\*\*ThrAspGluLysLysIleGluGluLys 486  
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 Db 1441 CCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAATAGAAGAAAAG 1500

Qy 487 LysAlaGlnIleValThrGluLysAsnThrSerThrLysThrSerAsnProPhePheVal 506  
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 Db 1501 AAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAACCCTTTTCTTGTA 1560

Qy 507 AlaAlaGlnAspSerGluThrAspTyrValThrThrAspAsnLeuThrLysValThrGlu 526  
 |||  
 Db 1561 GCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGTGACTGAG 1620

Qy 527 GluValValAlaAsnMetProGluGlyLeuThrProAspLeuValGlnGluAlaCysGlu 546  
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 Db 1621 GAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGTGAA 1680

Qy 547 SerGluLeuAsnGluValThrGlyThrLysIleAlaTyrGluThrLysMetAspLeuVal 566  
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 Db 1681 AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAATGGACTTGTT 1740

Qy 567 GlnThrSerGluValMetGlnGluSerLeuTyrProAlaAlaGlnLeuCysProSerPhe 586  
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 Db 1741 CAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCATTT 1800

Qy 587 GluGluSerGluAlaThrProSerProValLeuProAspIleValMetGluAlaProLeu 606  
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 Db 1801 GAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAAGCACCATTG 1860

Qy 607 AsnSerAlaValProSerAlaGlyAlaSerValIleGlnProSerSerSerProLeuGlu 626  
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 Db 1861 AATTCTGCAGTTCCTAGTGCTGGTGCTTCGTGATACAGCCAGCTCATCACCATTAGAA 1920

Qy 627 AlaSerSerValAsnTyrGluSerIleLysHisGluProGluAsnProProProTyrGlu 646  
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 Db 1921 GCTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCCACCATATGAA 1980

Qy 647 GluAlaMetSerValSerLeu---LysValSerGlyIleLysGluGluIleLysGluPro 665  
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 Db 1981 GAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAATTAAAGAGCCT 2040

Qy 666 GluAsnIleAsnAlaAlaLeuGlnGluThrGluAlaProTyrIleSerIleAlaCysAsp 685  
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 Db 2041 GAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCATGTGAT 2100

Qy 686 LeuIleLysGluThrLysLeuSerAlaGluProAlaProAspPheSerAspTyrSerGlu 705  
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 Db 2101 TTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGATTATTAGAA 2160

Qy 706 MetAlaLysValGluGlnProValProAspHisSerGluLeuValGluAspSerSerPro 725

Db	2161		ATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGATTCCTCACCT	2220
Qy	726		AspSerGluProValAspLeuPheSerAspAspSerIleProAspValProGlnLysGln	745
Db	2221		GATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAACAA	2280
Qy	746		AspGluThrValMetLeuValLysGluSerLeuThrGluThrSerPheGluSerMetIle	765
Db	2281		GATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGATA	2340
Qy	766		GluTyrGluAsnLysGluLysLeuSerAlaLeuProProGluGlyGlyLysProTyrLeu	785
Db	2341		GAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAGCCATATTTG	2400
Qy	786		GluSerPheLysLeuSerLeuAspAsnThrLysAspThrLeuLeuProAspGluValSer	805
Db	2401		GAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGATGAAGTTTCA	2460
Qy	806		ThrLeuSerLysLysGluLysIleProLeuGlnMetGluGluLeuSerThrAlaValTyr	825
Db	2461		ACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACTGCAGTTTAT	2520
Qy	826		SerAsnAspAspLeuPheIleSerLysGluAlaGlnIleArgGluThrGluThrPheSer	845
Db	2521		TCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAAACGTTTCA	2580
Qy	846		AspSerSerProIleGluIleIleAspGluPheProThrLeuIleSerSerLysThrAsp	865
Db	2581		GATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTTCTAAACTGAT	2640
Qy	866		SerPheSerLysLeuAlaArgGluTyrThrAspLeuGluValSerHisLysSerGluIle	885
Db	2641		TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCACAAAAGTGAAATT	2700
Qy	886		AlaAsnAlaProAspGlyAlaGlySerLeuProCysThrGluLeuProHisAspLeuSer	905
Db	2701		GCTAATGCCCCGGATGGAGCTGGGTCAATTGCCTGCACAGAATTGCCCCATGACCTTTCT	2760
Qy	906		LeuLysAsnIleGlnProLysValGluGluLysIleSerPheSerAspAspPheSerLys	925
Db	2761		TTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGACTTTTCTAAA	2820
Qy	926		AsnGlySerAlaThrSerLysValLeuLeuLeuProProAspValSerAlaLeuGlyHis	945
Db	2821		AATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCTTTGGCC---	2877
Qy	946		ThrGlnAlaGluIleGluSerIleValLysProLysValLeuGluLysGluAlaGluLys	965
Db	2878		ACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAAGCTGAGAAA	2937
Qy	966		LysLeuProSerAspThrGluLysGluAspArgSerProSerAlaIlePheSerAlaAsp	985
Db	2938		AAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAG	2997
Qy	986		LeuGlyLysThrSerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal	1005

Db 2998 CTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG 3057

Qy 1006 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal 1025  
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Db 3058 GTGTTTGGTGCCAGCCTATTCTGTGCTTTTCATTGACAGTATTACAGCATTGTGAGCGTA 3117

Qy 1026 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly 1045  
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Db 3118 ACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGT 3177

Qy 1046 ValIleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSer 1065  
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Db 3178 GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAATCT 3237

Qy 1066 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 1085  
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Db 3238 GAAGTTGCTATATCTGAGGAGTTGGTTTCAAGTACAGTAATTCTGCTCTTGGTCATGTG 3297

Qy 1086 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 1105  
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Db 3298 AACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG 3357

Qy 1106 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 1125  
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Db 3358 AAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACA 3417

Qy 1126 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 1145  
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Db 3418 CTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCCTGTTATTTATGAACGGCATCAG 3477

Qy 1146 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 1165  
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Db 3478 GCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA 3537

Qy 1166 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 1178  
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Db 3538 ATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAA 3576

RESULT 6

US-09-893-348-22

; Sequence 22, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

```
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22
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Alignment Scores:

Pred. No.:	0	Length:	3579
Score:	5810.00	Matches:	1159
Percent Similarity:	97.49%	Conservative:	4
Best Local Similarity:	97.15%	Mismatches:	14
Query Match:	98.09%	Indels:	16
DB:	9	Gaps:	3

US-09-830-972-29 (1-1178) x US-09-893-348-22 (1-3579)

Qy	1	MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln	20
Db	1	ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACCCGCGCCGAC	60
Qy	21	ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGlu	40
Db	61	CCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAGGAAGAAGAGGAGGAG	120
Qy	41	GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla	60
Db	121	GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGCCCGCC	180
Qy	61	AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp	80
Db	181	GCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCGGCGCGCCCTGATGGAC	240
Qy	81	PheGlyAsnAspPheValProProAlaProArgGlyProLeuProAlaAlaProProVal	100
Db	241	TTCGGAAATGACTTCGTGCCGCGGCGCCCGGGGACCCCTGCCGCGCGCTCCCCCGTC	300
Qy	101	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	120
Db	301	GCCCCGAGCGGCAGCCGTCTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCGCGCCA	360
Qy	121	SerProLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro	140
Db	361	TCCCCGCTGTCTGCTGCCGAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAGCCTCCG	420
Qy	141	AlaArgProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr	160
Db	421	GCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTGTGGACC	480

Qy	161	ProProAlaProAlaProAlaAlaProProSerThrProAlaAlaProLysArgArgGly	180
Db	481	CCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCGCCCAAGCGCAGGGGC	540
Qy	181	SerSerGlyAla-----ValVal	186
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Db	541	TCCTCGGGCTCAGTGGATGAGACCCTTTTGTCTCTCCTGCTGCATCTGAGCCTGTGATA	600
Qy	187	*****LysIleMetAspLeuLysGluGlnProGlyAsnThrIleSerAlaGly	206
		:::	
Db	601	CGCTCCTCTGCAGAAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTTCGGCTGGT	660
Qy	207	GlnGluAspPheProSerValLeuLeuGluThrAlaAlaSer***ProSerLeuSerPro	226
Db	661	CAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCTTCTCTCCTTCTCTGTCTCTCT	720
Qy	227	LeuSerAlaAlaSerPheLysGluHisGluTyrLeuGlyAsnLeuSerThrValLeuPro	246
Db	721	CTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACAGTATTACCC	780
Qy	247	ThrGluGlyThrLeuGlnGluAsnValSerGluAlaSerLysGluValSerGluLysAla	266
Db	781	ACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAAGGCA	840
Qy	267	LysThrLeuLeuIleAspArgAspLeuThrGluPheSerGluLeuGluTyrSerGluMet	286
Db	841	AAAACCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATACTCAGAAATG	900
Qy	287	GlySerSerPheSerValSerProLysAlaGluSerAlaValIleValAlaAsnProArg	306
Db	901	GGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCAAATCCTAGG	960
Qy	307	GluGluIleIleValLysAsnLysAspGluGluGluLysLeuValSerAsnAsnIleLeu	326
Db	961	GAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAATAACATCCTT	1020
Qy	327	His***GlnGlnGluLeuProThrAlaLeuThrLysLeuValLysGluAspGluValVal	346
Db	1021	CATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGATGAAGTTGTG	1080
Qy	347	SerSerGluLysAlaLysAspSerPheAsnGluLysArgValAlaValGluAlaProMet	366
Db	1081	TCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATG	1140
Qy	367	ArgGluGluTyrAlaAspPheLysProPheGluArgValTrpGluValLysAspSerLys	386
Db	1141	AGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAAGATAGTAAG	1200
Qy	387	GluAspSerAspMetLeuAlaAlaGlyGlyLysIleGluSerAsnLeuGluSerLysVal	406
Db	1201	GAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTGGAAGTAAAGTG	1260
Qy	407	AspLysLysCysPheAlaAspSerLeuGluGlnThrAsnHisGluLysAspSerGluSer	426
Db	1261	GATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAAGATAGTGAGAGT	1320

Qy 427 SerAsnAspAspThrSerPheProSerThrProGluGlyIleLysAspArgSerGlyAla 446  
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 Db 1321 AGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGATCGTCCAGGAGCA 1380

Qy 447 TyrIleThrCysAlaProPheAsnProAlaAlaThrGluSerIleAlaThrAsnIlePhe 466  
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 Db 1381 TATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCAACAAACATTTTT 1440

Qy 467 ProLeuLeuGluAspProThrSerGluAsn\*\*\*ThrAspGluLysLysIleGluGluLys 486  
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 Db 1441 CCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAATAGAAGAAAAG 1500

Qy 487 LysAlaGlnIleValThrGluLysAsnThrSerThrLysThrSerAsnProPhePheVal 506  
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 Db 1501 AAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAACCCTTTTCTTGTA 1560

Qy 507 AlaAlaGlnAspSerGluThrAspTyrValThrThrAspAsnLeuThrLysValThrGlu 526  
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 Db 1561 GCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGTGACTGAG 1620

Qy 527 GluValValAlaAsnMetProGluGlyLeuThrProAspLeuValGlnGluAlaCysGlu 546  
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 Db 1621 GAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGTGAA 1680

Qy 547 SerGluLeuAsnGluValThrGlyThrLysIleAlaTyrGluThrLysMetAspLeuVal 566  
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 Db 1681 AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAATGGACTTGTT 1740

Qy 567 GlnThrSerGluValMetGlnGluSerLeuTyrProAlaAlaGlnLeuCysProSerPhe 586  
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 Db 1741 CAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCATTT 1800

Qy 587 GluGluSerGluAlaThrProSerProValLeuProAspIleValMetGluAlaProLeu 606  
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 Db 1801 GAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAAGCACCATTG 1860

Qy 607 AsnSerAlaValProSerAlaGlyAlaSerValIleGlnProSerSerSerProLeuGlu 626  
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 Db 1861 AATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTAGAA 1920

Qy 627 AlaSerSerValAsnTyrGluSerIleLysHisGluProGluAsnProProProTyrGlu 646  
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 Db 1921 GCTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCCACCATATGAA 1980

Qy 647 GluAlaMetSerValSerLeu---LysValSerGlyIleLysGluGluIleLysGluPro 665  
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 Db 1981 GAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAATTAAAGAGCCT 2040

Qy 666 GluAsnIleAsnAlaAlaLeuGlnGluThrGluAlaProTyrIleSerIleAlaCysAsp 685  
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 Db 2041 GAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCATGTGAT 2100

Qy 686 LeuIleLysGluThrLysLeuSerAlaGluProAlaProAspPheSerAspTyrSerGlu 705  
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Db	2161		ATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGATTCCTCACCT	2220
Qy	726		AspSerGluProValAspLeuPheSerAspAspSerIleProAspValProGlnLysGln	745
Db	2221		GATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAACAA	2280
Qy	746		AspGluThrValMetLeuValLysGluSerLeuThrGluThrSerPheGluSerMetIle	765
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Qy	766		GluTyrGluAsnLysGluLysLeuSerAlaLeuProProGluGlyGlyLysProTyrLeu	785
Db	2341		GAAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAGCCATATTTG	2400
Qy	786		GluSerPheLysLeuSerLeuAspAsnThrLysAspThrLeuLeuProAspGluValSer	805
Db	2401		GAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGATGAAGTTTCA	2460
Qy	806		ThrLeuSerLysLysGluLysIleProLeuGlnMetGluGluLeuSerThrAlaValTyr	825
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Db	2521		TCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAAACGTTTTCA	2580
Qy	846		AspSerSerProIleGluIleIleAspGluPheProThrLeuIleSerSerLysThrAsp	865
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Qy	866		SerPheSerLysLeuAlaArgGluTyrThrAspLeuGluValSerHisLysSerGluIle	885
Db	2641		TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATT	2700
Qy	886		AlaAsnAlaProAspGlyAlaGlySerLeuProCysThrGluLeuProHisAspLeuSer	905
Db	2701		GCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACAGAATTGCCCCATGACCTTTCT	2760
Qy	906		LeuLysAsnIleGlnProLysValGluGluLysIleSerPheSerAspAspPheSerLys	925
Db	2761		TTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGACTTTTCTAAA	2820
Qy	926		AsnGlySerAlaThrSerLysValLeuLeuLeuProProAspValSerAlaLeuGlyHis	945
Db	2821		AATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCTTTGGCC---	2877
Qy	946		ThrGlnAlaGluIleGluSerIleValLysProLysValLeuGluLysGluAlaGluLys	965
Db	2878		ACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAAGCTGAGAAA	2937
Qy	966		LysLeuProSerAspThrGluLysGluAspArgSerProSerAlaIlePheSerAlaAsp	985
Db	2938		AAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAG	2997
Qy	986		LeuGlyLysThrSerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal	1005

36	703	38.0	1520	15	US-10-084-817-333	Sequence 333, App
37	699	37.8	1473	15	US-10-205-194-128	Sequence 128, App
38	695	37.6	422	9	US-09-960-352-8477	Sequence 8477, Ap
39	678	36.6	1766	10	US-09-809-391-254	Sequence 254, App
40	678	36.6	1766	10	US-09-882-171-254	Sequence 254, App
41	678	36.6	1766	17	US-10-164-861-254	Sequence 254, App
42	677	36.6	1915	17	US-10-276-774-980	Sequence 980, App
43	674	36.4	1668	9	US-09-765-205-25	Sequence 25, Appl
44	674	36.4	2768	18	US-10-723-860-6867	Sequence 6867, Ap
45	672	36.3	422	9	US-09-960-352-11567	Sequence 11567, A

# ALIGNMENTS

## RESULT 1

US-09-789-386-5

Sequence 5, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1122  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-5

## Alignment Scores:

Pred. No.:	5.13e-152	Length:	1122
Score:	1829.00	Matches:	360
Percent Similarity:	96.51%	Conservative:	0
Best Local Similarity:	96.51%	Mismatches:	1
Query Match:	98.86%	Indels:	12
DB:	9	Gaps:	1

SEQ29 (1-361) x US-09-789-386-5 (1-1122)

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Qy	21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGlu	40
Db	61 CCCGCGTTCAAGTACAGTTCGTGAGGGAGCCCGAGGACGAGGAGGAAGAAGAGGAGGAG	120



Qy	41	GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla	60
Db	121	GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGCCCCGCC	180
Qy	61	AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp	80
Db	181	GCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCGGCGCGCCCCCTGATGGAC	240
Qy	81	PheGlyAsnAspPheValProProAlaProArgGlyProLeuProAlaAlaProProVal	100
Db	241	TTCGGAAATGACTTCGTGCCCGCGCGCCCCGGGGACCCCTGCCGCGCGCTCCCCCGCTC	300
Qy	101	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	120
Db	301	GCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTCCCCGCGCCA	360
Qy	121	SerProLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro	140
Db	361	TCCCCGCTGTCTGCTGCCGAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAGCCTCCG	420
Qy	141	AlaArgProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr	160
Db	421	GCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTGTGGACC	480
Qy	161	ProProAlaProAlaProAlaAlaProProSerThrSer-----	173
Db	481	CCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCGCGCCCAAGCGCAGGGGC	540
Qy	174	-----ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal	188
Db	541	TCCTCGGGCTCAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG	600
Qy	189	ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal	208
Db	601	GTGTTTGGTGCCAGCCTATTCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTA	660
Qy	209	ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly	228
Db	661	ACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGT	720
Qy	229	ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer	248
Db	721	GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCATATCTGGAATCT	780
Qy	249	GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal	268
Db	781	GAAGTTGCTATATCTGAGGAGTTGGTTTCAAGTACAGTAATTCTGCTCTTGGTCATGTG	840
Qy	269	AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu	288
Db	841	AACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG	900
Qy	289	LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr	308
Db	901	AAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACA	960
Qy	309	LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln	328

```

          |||
Db      961 CTACTGATTTGGCTCTCATTCTACTCTTCAGTGTCCTGTTATTTATGAACGGCATCAG 1020
Qy      329 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 348
          |||
Db      1021 GCACAGATAGATCATTATCTAGGACTTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAA 1080
Qy      349 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 361
          |||
Db      1081 ATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAA 1119

```

RESULT 2

US-09-765-205-5

; Sequence 5, Application US/09765205

; Patent No. US20020034800A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Li

; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

; FILE REFERENCE: 1458.004/200130.449

; CURRENT APPLICATION NUMBER: US/09/765,205

; CURRENT FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: US/09/212,440

; PRIOR FILING DATE: 1998-12-16

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 1610

; TYPE: DNA

; ORGANISM: human

US-09-765-205-5

Alignment Scores:

Pred. No.:	8.25e-152	Length:	1610
Score:	1829.00	Matches:	360
Percent Similarity:	96.51%	Conservative:	0
Best Local Similarity:	96.51%	Mismatches:	1
Query Match:	98.86%	Indels:	12
DB:	9	Gaps:	1

SEQ29 (1-361) x US-09-765-205-5 (1-1610)

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Qy      1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20
          |||
Db      132 ATGGAAGACCTGGACCACTCTCCTCTGGTCTCGTCTCGGACAGCCACCCCGGCCGCAG 191
Qy      21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGlu 40
          |||
Db      192 CCCGCGTTCAAGTACCACTTCGTGAGGGAGCCCGAGGACGAGGAGGAAGAAGAGGAGGAG 251
Qy      41 GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla 60
          |||
Db      252 GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGCCCGCC 311
Qy      61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
          |||
Db      312 GCCGGGCTGTCCGCGGCCCACTGCCACCGCCCCTGCCGCCGGCGCGCCCCTGATGGAC 371

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Db 3565 AAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTG 3624  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 3625 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG 3684  
 Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 3685 GCTCTCATTTCACCTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3744  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 3745 CATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3804  
 Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
 ||||||||||||||||||||||||||||  
 Db 3805 ATCCCTGGATTGAAGCGCAAAGCTGAA 3831

RESULT 2

US-08-700-607-2

; Sequence 2, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 799 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-2
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Alignment Scores:

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Pred. No.:      4.77e-120      Length:      799
Score:          927.00         Matches:     188
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:     0
Query Match:    99.57%        Indels:        0
DB:             2             Gaps:         0
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-700-607-2 (1-799)

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Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
      |||
Db     108 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 167

Qy     22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
      |||
Db     168 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 227

Qy     42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
      |||
Db     228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287

Qy     62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
      |||
Db     288 CAGAAATCAGATGAAGGCCACCCATTGAGGGCATATCTGGAATCTGAAGTTGCTATATCT 347

Qy     82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
      |||
Db     348 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 407

Qy    102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
      |||
Db     408 GAAGTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 467

Qy    122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
      |||
Db     468 ATGTGGGTATTTACCTATGTTGGTGCCTGTGTTAATGGTCTGACACTACTGATTTTGGCT 527

Qy    142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
      |||
Db     528 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587

Qy    162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db     588 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 647

Qy    182 ProGlyLeuLysArgLysAlaGlu 189
      |||
Db     648 CCTGGATTGAAGCGCAAAGCTGAA 671
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RESULT 3

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; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-810-653-20

Query Match          99.1%; Score 921; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.4e-81;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2  VVDLLYWRDIKKTGVFGASLFLLLSLTVPFISVTVAYIALALLSVTISFRIYKGVIOA 61
Db  173 VVDLLYWRDIKKTGVFGASLFLLLSLTVPFISVTVAYIALALLSVTISFRIYKGVIOA 232

Qy  62  QKSDGHPFRAYLESEVAISELKVQYNSALGHVNSTIKELRFLVDDLVDSLKFV 121
Db  233 QKSDGHPFRAYLESEVAISELKVQYNSALGHVNSTIKELRFLVDDLVDSLKFV 292

Qy  122 MWVFTYVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYGLANKSVKDMAKIOAK 181
Db  293 MWVFTYVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYGLANKSVKDMAKIOAK 352

Qy  182 PGLKRXAD 189
Db  353 PGLKRXAD 360

RESULT 8
US-10-633-423-10
; Sequence 10, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023.US00
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-633-423-10

Query Match          99.1%; Score 917; DB 16; Length 1162;
Best Local Similarity 98.9%; Pred. No. 2.4e-80;
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1  SVVDLLYWRDIKKTGVFGASLFLLLSLTVPFISVTVAYIALALLSVTISFRIYKGVIOA 60
Db  974 SVVDLLYWRDIKKTGVFGASLFLLLSLTVPFISVTVAYIALALLSVTISFRIYKGVIOA 1033

Qy  61  IQKSDGHPFRAYLESEVAISELKVQYNSALGHVNSTIKELRFLVDDLVDSLKFV 120
Db  1034 IQKSDGHPFRAYLESEVAISELKVQYNSALGHVNSTIKELRFLVDDLVDSLKFV 1093

Qy  121 LMWVFTYVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYGLANKSVKDMAKIOAK 180
Db  1094 LMWVFTYVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYGLANKSVKDMAKIOAK 1153

Qy  181 IPGLKRXAD 189
Db  1154 IPGLKRXAD 1162

RESULT 10
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-789-386-2

Query Match          98.2%; Score 908; DB 9; Length 1192;
Best Local Similarity 97.4%; Pred. No. 1.9e-79;

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```

Db  1154 IPGLKRXAD 1162

RESULT 9
US-10-427-741-10
; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
; GENERAL INFORMATION:
; APPLICANT: Yamashita, Masaya
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023
; CURRENT APPLICATION NUMBER: US/10/427,741
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-427-741-10

Query Match          99.1%; Score 917; DB 16; Length 1162;
Best Local Similarity 98.9%; Pred. No. 2.4e-80;
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1  SVVDLLYWRDIKKTGVFGASLFLLLSLTVPFISVTVAYIALALLSVTISFRIYKGVIOA 60
Db  974 SVVDLLYWRDIKKTGVFGASLFLLLSLTVPFISVTVAYIALALLSVTISFRIYKGVIOA 1033

Qy  61  IQKSDGHPFRAYLESEVAISELKVQYNSALGHVNSTIKELRFLVDDLVDSLKFV 120
Db  1034 IQKSDGHPFRAYLESEVAISELKVQYNSALGHVNSTIKELRFLVDDLVDSLKFV 1093

Qy  121 LMWVFTYVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYGLANKSVKDMAKIOAK 180
Db  1094 LMWVFTYVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYGLANKSVKDMAKIOAK 1153

Qy  181 IPGLKRXAD 189
Db  1154 IPGLKRXAD 1162

RESULT 10
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-789-386-2

Query Match          98.2%; Score 908; DB 9; Length 1192;
Best Local Similarity 97.4%; Pred. No. 1.9e-79;

```

Score:	931.00	Matches:	189
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-789-386-1 (1-3579)

QY	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
DB	3010	TCAGTTGTTGCACCTCTGTACTGAGAGACATTAAAGAAGACTGAGTGGTGTGGTGCC	3069
QY	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
DB	3070	AGCTATTCTGCTGCTTTCAATGACAGTATTGACCAATGTGAGCGGTAAACAGCTACATT	3129
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
DB	3130	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT	3189
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
DB	3190	ATCCAGAAATCAGATGAAGGCCCAACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA	3249
QY	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
DB	3250	TCTGAGGAGTTGGTTCCAGAAGTACAGTAATCTCTGCTCTTGGTCATGTGAACTGCACGATA	3309
QY	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
DB	3310	AAGGAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAATG	3369
QY	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
DB	3370	TTGATGTGGGTATTTACCTATGTTGGTGGCTTGTTTAATGGTCTGACACTCTGATTTTG	3429
QY	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
DB	3430	GCTCTCATTTTCACTCTTCAGTGTCTCTGTATTATTATGAACGGCATCAGCGCGAGTAGAT	3489
QY	161	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaIleIleGlnAlaLys	180
DB	3490	CATTATCTAGGACTTGCAANTAAGATGTTAAGATGCTATGGCTAAATATCCAGCAAA	3549
QY	181	IleProGlyLeuLysArgLysAlaGlu	189
DB	3550	ATCCCTCGATTGAAGCGCAAGCTGAA	3576

RESULT 8  
US-09-893-348-22  
Sequence 22, Application US/09893348  
Patent No. US20020072493A1  
GENERAL INFORMATION:  
APPLICANT: EISENBERG-SCHWARTZ, Michal  
APPLICANT: COHEN, Irun R.  
APPLICANT: BESERMAN, Pierre  
APPLICANT: MOSONEGO, Alon  
APPLICANT: MOALEM, Gila  
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
FILE REFERENCE: EIS-SCHWARTZ=2A  
CURRENT APPLICATION NUMBER: US/09/893,348  
CURRENT FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: US 09/314,161  
PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: US 09/218,277  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: PCT/US98/14715  
PRIOR FILING DATE: 1998-07-21  
PRIOR APPLICATION NUMBER: IL 124500  
PRIOR FILING DATE: 1998-05-19  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 22

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; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22

Alignment Scores:
Pred. No.: 4.33e-106
Score: 931.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9
Length: 3579
Matches: 189
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-893-348-22 (1-3579)

QY	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyVala	20
DB	3010	TCAGTTGTTGACCTCCTCTACTGCGAGACATTAGAAGACTGGAGTGGTGTGGTGCC	3069
QY	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
DB	3070	AGCCTATTCTCTGCTGCTTCTCATTCGACGATTTCAGCATTGTGAGCGTAACAGCCTACATT	3129
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
DB	3130	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAGGGGTGTGATCCNAGCT	3189
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
DB	3190	ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGATCTGAAGTTGCTATA	3249
QY	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
DB	3250	TCTCAGGAGTTGGTTTCAGAAGTACAGTAATTTCTGCTCTTGTCATGTGAACGTGCACGATA	3309
QY	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
DB	3310	AAGGAATCAGGCCCTCTCTTAGTTAGTGAATTTAGTTGATCTCTGAAGTTTGCAGTG	3369
QY	121	LeuMetTrpValPheThrTyrValGlyValaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
DB	3370	TTGATGTGGGTATTATCCTATGTTGGTGCCCTTGTTTAATGGTCTGCACACTACTGATTTTG	3429
QY	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
DB	3430	GCTCTCATTTTCACTCTTTCAGTGTCTCTGTTATTATTATGAACGGCATCAGGGCGCAGATAGAT	3489
QY	161	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
DB	3490	CATTATCTAGGACTTGCATAATAGAATGTTAAGATGCTATGCTTAAATCCARGCAAA	3549
QY	181	IleProGlyLeuLysArgLysAlaGlu	189
DB	3550	ATCCCTGGATTGAAGGCCAAGCTGAA	3576

RESULT 7  
US-10-267-502-212  
Sequence 212, Application US/10267502  
Publication No. US20040071700A1  
GENERAL INFORMATION:  
APPLICANT: Kim, Jaeseob  
APPLICANT: Galant, Ron  
TITLE OF INVENTION: Obesity Linked Genes  
FILE REFERENCE: LSD-07416  
CURRENT APPLICATION NUMBER: US/10/267,502  
CURRENT FILING DATE: 2003-01-27  
NUMBER OF SEQ ID NOS: 439  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 212

Tue Jun 21 16:29:13 2005

PRIOR APPLICATION NUMBER: US 09/218,277  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: PCT/US98/14715  
PRIOR FILING DATE: 1998-07-21  
PRIOR APPLICATION NUMBER: IL 124500  
PRIOR FILING DATE: 1998-05-19  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 23  
LENGTH: 1192  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-893-348-23

Query Match 100.0%; Score 931; DB 9; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOA 60  
DB 1004 SVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRLFLVDDLVDSLKFAV 120  
DB 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRLFLVDDLVDSLKFAV 1123  
QY 121 LMWVFTYVGCALFNGLTLLILALISLFSVPVYIYERHOAQIDHYLGLANKVNDAMAKIOAK 180  
DB 1124 LMWVFTYVGCALFNGLTLLILALISLFSVPVYIYERHOAQIDHYLGLANKVNDAMAKIOAK 1183  
QY 181 IPGLKKEAE 189  
DB 1184 IPGLKKEAE 1192

RESULT 4

US-09-972-599A-6  
Sequence 6, Application US/09972599A  
Patent No. US20020077295A1  
GENERAL INFORMATION:  
APPLICANT: STRITTMATTER, STEPHEN M.  
TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
FILE REFERENCE: C077 CIP US  
CURRENT APPLICATION NUMBER: US/09/972,599A  
CURRENT FILING DATE: 2001-10-06  
PRIOR APPLICATION NUMBER: PCT/US01/01041  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 09/758,140  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 60/236,378  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/207,366  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/175,707  
PRIOR FILING DATE: 2000-01-12  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: Patent in ver. 2.1  
SEQ ID NO 6  
LENGTH: 1192  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-972-599A-6

Query Match 100.0%; Score 931; DB 9; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOA 60  
DB 1004 SVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRLFLVDDLVDSLKFAV 120

1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRLFLVDDLVDSLKFAV 1123  
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1124 LMWVFTYVGCALFNGLTLLILALISLFSVPVYIYERHOAQIDHYLGLANKVNDAMAKIOAK 1183  
181 IPGLKKEAE 189  
1184 IPGLKKEAE 1192

RESULT 2  
US-09-758-140-6  
Sequence 6, Application US/09758140  
Patent No. US20020012965A1  
GENERAL INFORMATION:  
APPLICANT: Strittmatter, Stephen M.  
TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth  
FILE REFERENCE: 44574-5073-US  
CURRENT APPLICATION NUMBER: US/09/758,140  
CURRENT FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/175,707  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: US 60/207,366  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 60/236,378  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent in ver. 2.1  
SEQ ID NO 6  
LENGTH: 1192  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-758-140-6

Query Match 100.0%; Score 931; DB 9; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOA 60  
DB 1004 SVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRLFLVDDLVDSLKFAV 120  
DB 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRLFLVDDLVDSLKFAV 1123  
QY 121 LMWVFTYVGCALFNGLTLLILALISLFSVPVYIYERHOAQIDHYLGLANKVNDAMAKIOAK 180  
DB 1124 LMWVFTYVGCALFNGLTLLILALISLFSVPVYIYERHOAQIDHYLGLANKVNDAMAKIOAK 1183  
QY 181 IPGLKKEAE 189  
DB 1184 IPGLKKEAE 1192

RESULT 3

US-09-893-348-23  
Sequence 23, Application US/09893348  
Patent No. US20020072493A1  
GENERAL INFORMATION:  
APPLICANT: EISENBACH-SCHWARTZ, Michal  
APPLICANT: COHEN, Itzhak R.  
APPLICANT: BESERMAN, Pierre  
APPLICANT: MOSONOGO, Alon  
APPLICANT: MOALEM, Gila  
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
FILE REFERENCE: EIS-SCHWARTZ=2A  
CURRENT APPLICATION NUMBER: US/09/893,348  
CURRENT FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: US 09/314,161  
PRIOR FILING DATE: 1999-05-19

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 7.13706 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925  
Sequence: 1 SVVDLLYWRDKTGVFGASLFLSLVTSVTVATIALLSVTISFRIYKGVIOAI 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfile1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	904	97.7	199	2	US-08-700-607-1
2	904	97.7	201	4	US-09-949-016-9124
3	679	73.4	208	2	US-08-700-607-7
4	679	73.4	356	2	US-08-700-607-6
5	679	73.4	439	4	US-09-949-016-9180
6	679	73.4	776	2	US-08-700-607-5
7	679	73.4	776	4	US-09-949-016-6998
8	665	71.9	267	2	US-08-700-607-8
9	625.5	67.6	192	4	US-09-949-016-8859
10	539.5	58.3	168	4	US-09-149-476-563
11	518	56.0	219	4	US-09-270-767-45132
12	516	55.8	241	2	US-08-700-607-3
13	475	51.4	588	4	US-09-949-016-7290
14	286	30.9	92	4	US-09-149-476-411
15	246	26.6	114	4	US-09-513-999C-7861
16	142	15.4	374	4	US-09-248-796A-16008
17	100	10.8	80	3	US-08-905-223-411
18	95	10.3	468	4	US-08-487-596-8
19	95	10.3	468	4	US-08-660-451A-8
20	94	10.2	382	4	US-09-949-016-11596
21	88.5	9.6	1278	4	US-09-462-136-2
22	88.5	9.6	1318	4	US-09-949-016-10152
23	86.5	9.4	592	4	US-09-134-000C-5477
24	86	9.3	414	4	US-08-956-171B-5246
25	86	9.3	414	4	US-08-781-986A-5246
26	85.5	9.2	1051	3	US-09-134-001C-5005
27	84.5	9.1	593	4	US-09-328-352-4866

28	83	9.0	459	4	US-09-602-787A-302	Sequence 302, App
29	82.5	8.9	410	4	US-09-583-110-3963	Sequence 3963, Ap
30	82.5	8.9	424	4	US-09-107-433-5202	Sequence 5202, Ap
31	82	8.9	614	4	US-09-540-236-2858	Sequence 2858, Ap
32	81.5	8.8	280	4	US-09-543-681A-6175	Sequence 6175, Ap
33	81.5	8.8	383	4	US-09-248-796A-14833	Sequence 14833, A
34	81	8.8	744	4	US-09-785-381-1	Sequence 1, Appli
35	81	8.8	744	4	US-09-785-381-3	Sequence 3, Appli
36	80.5	8.7	252	4	US-09-583-110-4880	Sequence 4880, Ap
37	80.5	8.7	257	4	US-09-107-433-4818	Sequence 4818, Ap
38	80.5	8.7	598	2	US-08-853-659A-53	Sequence 53, Appl
39	79	8.5	289	4	US-09-540-236-2019	Sequence 2019, Ap
40	79	8.5	554	4	US-09-252-991A-27968	Sequence 27968, A
41	78.5	8.5	743	4	US-09-724-653-8	Sequence 8, Appli
42	78.5	8.5	748	3	US-09-061-764A-19	Sequence 19, Appl
43	78.5	8.5	808	4	US-09-917-254-52	Sequence 52, Appl
44	78	8.4	231	4	US-09-198-452A-419	Sequence 419, App
45	78	8.4	420	3	US-09-134-001C-3805	Sequence 3805, Ap

## ALIGNMENTS

RESULT 1  
US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5859768  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 199 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: Consensus  
; CLONE: 700-607-1  
; US-08-700-607-1

Query Match 97.7%; Score 904; DB 2; Length 199;

Best Local Similarity 97.3%; Pred. No. 7.9e-89; Indels 0; Gaps 0;

Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VVDLLYWRDKTGVFGASLFLSLVTSVTVATIALLSVTISFRIYKGVIOAI 61



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Db      12 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY      62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
Db      72 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131
QY      122 MVFTYVVGALFNGLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAWAKIOAKI 181
Db      132 MVFTYVVGALFNGLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAWAKIOAKI 191
QY      182 PGLKRXAD 189
Db      192 PGLKRXAE 199

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RESULT 2
US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124

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Query Match      97.7%; Score 904; DB 4; Length 201;
Best Local Similarity 97.3%; Pred. No. 8e-89;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
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QY      62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
Db      74 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 133
QY      122 MVFTYVVGALFNGLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAWAKIOAKI 181
Db      134 MVFTYVVGALFNGLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAWAKIOAKI 193
QY      182 PGLKRXAD 189
Db      194 PGLKRXAE 201

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RESULT 3
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

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Query Match      73.4%; Score 679; DB 2; Length 208;
Best Local Similarity 67.9%; Pred. No. 1e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY      3 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQ 62
Db      22 IDLYWRDIKQTGIVFGSFLLLSLTVFSIVSVVAYIALAALSATISFRIYKSVLQAVQ 81
QY      63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 122
Db      82 KTDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 141
QY      123 MVFTYVVGALFNGLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAWAKIOAKIP 182
Db      142 WLTIVVGALFNGLTLLMAVSMFTLPVVVYKHQAQIDQYGLVTRHINAVVAKIOAKIP 201
QY      183 GLKRXAD 189
Db      202 GAKRXAE 208

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RESULT 4
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

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122 MetTTPValPheThrTyValGlyAlaLeuPheAenGlyLeuThrLeuLeuAla 141  
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142 LeuLeuSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHis 161  
528 CTCATTTCACCTCTTCAGTGTTCCTGTTATTATGACGGCATCAGGCACAGATGATCAT 587  
162 TyLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
588 TATCTAGGACTTGCATTAAGATGTTAAAGATGCTATGCTGCTAAATCCAAAGCAAAATC 647  
182 ProGlyLeuLysArgLysAlaAsp 189  
648 CTGGATTGAAGCGCAAGCTGAA 671

RESULT 48  
BC007109  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
ORIGIN

BC007109  
Homo sapiens reticulon 4, transcript variant 3, mRNA (cdna clone IMAGE:4291127), complete cds.  
BC007109.1 GI:13937989  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1079)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klautner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Loquellano, N.A., Peters, G.J., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., McSwain, P.J.; Abramson, R.D., Mullahy, S.J., Bosak, S.A., Richards, S., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vallalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Schmechel, J., Myers, R.M., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Smal, D.E., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smal, D.E., Schmechel, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1079)  
Straussberg, R.  
Direct Submission  
Submitted (30-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue procurement: CLONTECH  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found

RESULT 12  
US-09-892-348-23  
sequence 23, Application US/09893348  
Patent No. US20020072493A1  
GENERAL INFORMATION:  
APPLICANT: EISENBACH-SCHWARTZ, Michael  
APPLICANT: COHEN, Irm R.  
APPLICANT: BESERMAN, Pierre  
APPLICANT: MOSONEGO, Alon

```

RESULT 31
US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US2002007795A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMAYER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

```

Query Match 98.2%; Score 908; DB 9; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 1.9e-79;  
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-660-946-2

```

```

Alignment Scores:
Pred. No.: 2 98e-100 Length: 799
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 18 Gaps: 0

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US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-660-946-2 (1-799)

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLeuValPheGlyAlaSer 21
DB 108 GTTGTGACCTCTCTGCTGAGAGACATTAAAGAGCTGGAGTGGTGTGGTGGCCAGC 167
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 168 CTAATTCCTGCTCTCTCATTCAGCAGTATTTCAGCAGTATTGAGCGGTAAACAGCTTACATTGCC 227
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLeuGlyValIleGlnAlaIle 61
DB 228 TTGGCCCTCTCTCTGTGACCATGCTTTAGGATATACAGGGGTGATCAAGCTATC 287
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 288 CAGAAATCAGATGAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATGCTATATCT 347
QY 82 GluGluLeuValGlnLysTyrSerIleValSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 348 GAGGAGTGGTTCAGAAAGTACAGTAATTCCTGCTCTGGTTCATGCTGCAAGTAAAG 407
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 408 GAACCTCAGCGGCTCTCTCTAGTATGATTTAGTATGATTTCTGCAAGTTTCAGTGTG 467
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 468 ATGTGGGTATTACCTATGCTGTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 527
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 528 CTCATTTCACCTCTTCAGTGTCTCTGTTATTTATGAACCGCATCAGGCACAGATAGCAT 587
QY 162 TyrLeuGlyLeuAlaAsnLysSerValIleAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 588 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 647
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 648 CTTGGATTGAGCGCAAGCTGAA 671

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RESULT 21

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US-09-789-386-5
Sequence 5, Application US/09789386
Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHAŁOVICH, DAVID
; APPLICANT: PRINJHA, REBINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1

```

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; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-5

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Alignment Scores:
Pred. No.: 5.08e-100 Length: 1122
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 9 Gaps: 0

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US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-789-386-5 (1-1122)

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLeuValPheGlyAlaSer 21
DB 556 GTTGTGACCTCTCTGCTGAGAGACATTAAAGAGCTGGAGTGGTGTGGTGGCCAGC 615
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 616 CTAATTCCTGCTCTCTCATTCAGCAGTATTTCAGCAGTATTGAGCGGTAAACAGCTTACATTGCC 675
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 676 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCAAGCTATC 735
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 736 CAGAAATCAGATGAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATGCTATATCT 795
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 796 GAGGAGTGGTTCAGAAAGTACAGTAATTCCTGCTCTGGTTCATGTAAGTAAAG 855
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 856 GAACCTCAGCGGCTCTCTCTAGTATGATTTAGTATGATTTCTGCAAGTTTCAGTGTG 915
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 916 ATGTGGGTATTACCTATGCTGTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 975
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 976 CTCATTTCACCTCTTCAGTGTCTCTGTTATTTATGAACCGCATCAGGCACAGATAGCAT 1035
QY 162 TyrLeuGlyLeuAlaAsnLysSerValIleAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 1036 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1095
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 1096 CTTGGATTGAGCGCAAGCTGAA 1119

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RESULT 22

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US-10-175-523-156
Sequence 156, Application US/10175523
Publication No. US2003009264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal

```

QY	1126	LIIILALISLFSVPVIERHQAOIDHYLGIANKNVDMAKIQAKIPGLKRKAEE	1178
DH	1140	LIIILALISLFSVPVIERHQAOIDHYLGIANKNVDMAKIQAKIPGLKRKAEE	1192

```

RESULT-4
US-09-789-386-2
Sequence 2, Application US/09789386
Patent No. US2002010124A1
GENERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
APPLICANT: PRINOVAT, RABINOVICH-KUMAR
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30165-C1
CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: U.K. 9916998.1
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: U.K. 9816024.5
PRIOR FILING DATE: 1998-07-22
PRIOR APPLICATION NUMBER: US 09/359,208
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1192
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-789-386-2

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	Query Match	98.1%;	Score 5810;	DB 9;	Length 1192;	
	Best Local Similarity	97.2%;	Pred. No. 5.9e-261;			3
	Matches 1159;	Conservative	4; Mismatches 14;	Indels 16;	Gaps 3;	
QY	1	MEDLDQSPLVSSDSPRPPOPAKFKQFVREPEDDEEEEEEEDEDEDLBELEVLERKPA	60			
DB	1	MEDLDQSPLVSSDSPRPPOPAKFKQFVREPEDDEEEEEEEDEDEDLBELEVLERKPA	60			
QY	61	AGLSAAPVPPTAAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPRQPQSDWSPVSSTVPAP	120			
DB	61	AGLSAAPVPTAAPAAGAPLMDFGNDFVPPAPRGPLPAAFPVAPPEKPQSDWPFSVSTVPAP	120			
QY	121	SPLSAAAASPSKLPEDDDEPPARPPPPPASPQAPBPVMTTPAPAPAAPPSTTAAAPKRGR	180			
DB	121	SPLSAAAASPSKLPEDDDEPPARPPPPPASPQAPBPVMTTPAPAPAAPPSTTAAAPKRGR	180			
QY	181	SSGA-----VVXXXXXKMDLKQPGNTISAGQDPFBSVLLETAAASKPSLSP	226			
DB	181	SSGSVDETTLFALPAASEPVIRSAEENMDLKQPGNTISAGQDPFBSVLLETAAASLSP	240			
QY	227	LSAASFKEHYLGNLSTVLTPTGTGLQBNVSEAKSVSEKATLLIDRLTFEPSELEYSEM	286			
DB	241	LSAASFKEHYLGNLSTVLTPTGTGLQBNVSEAKSVSEKATLLIDRLTFEPSELEYSEM	300			
QY	287	GSPFSVSPKASAVIVANPREEIIVKNKDDEEKLVSNILHQQELPTALTCLKVEDEVV	346			
DB	301	GSPFSVSPKASAVIVANPREEIIVKNKDDEEKLVSNILHQQELPTALTCLKVEDEVV	360			
QY	347	SSEKAKOSFNKRVAVAPAMREEYADPKPERVVEVKDKESDMDMLAAGKIESNLESKV	406			
DB	361	SSEKAKOSFNKRVAVEAPMREEYADPKPERVVEVKDKESDMDMLAAGKIESNLESKV	420			
QY	407	DKKCFADSLQTNHEKODESSNDDTSPSTPEGIKDRSGAYITTCAPNPAAATESIATNIF	466			
DB	421	DKKCFADSLQTNHEKODESSNDDTSPSTPEGIKDRPGAYITTCAPNPAAATESIATNIP	480			
QY	467	PILEDPTSENKTDEKKIEBKKAQIVTEKNTSTKTSNPFVAADOSETDYVTDLNKVITE	526			
DB	481	PILEGPTSENKTDEKKIEBKKAQIVTEKNTSTKTSNPFVAADOSETDYVTDLNKVITE	540			
QY	527	EYVANMPGEGITPDLOVAECESFLNEVTGKIAYETKMIDLVTQSEVMQESLYPAAQLCPSP	586			
DB	541	EYVANMPGEGITPDLOVAECESFLNEVTGKIAYETKMIDLVTQSEVMQESIYPAAQLCPSP	600			

587	QY	ESEATPSPVLPOIYVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYIESIKHEPNPPPYE	660
601	DB	ESEATPSPVLPOIYVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYIESIKHEPNPPPYE	705
647	QY	EAMSVSL-KVSGIKSEIKEPENINAALOETEAPYISICDLIKETKLGAEPAPFSDYSE	720
661	DB	EAMSVSLKVKVSGIKSEIKEPENINAALOETEAPYISICDLIKETKLGAEPAPFSDYSE	765
706	QY	MAKVEQVPDHSDELVDSDSPDSEPDVDFSDDISIPVPOKQDQDVTMLVKESLTETSFESMI	780
721	DB	MAKVEQVPDHSDELVDSDSPDSEPDVDFSDDISIPVPOKQDQDVTMLVKESLTETSFESMI	825
766	QY	EYENKEKLSALPEGGKPYLESFKLSLDNTKOTLLPDEVSTLSKKEKIPLOMBELSTAVY	840
781	DB	EYENKEKLSALPEGGKPYLESFKLSLDNTKOTLLPDEVSTLSKKEKIPLOMBELSTAVY	885
826	QY	SNDLDFISKQAQIRETETPDSQSPIIIDEFPPTLSSKTDSPSKLAREYTDLEVSHKSEI	900
841	DB	SNDLDFISKQAQIRETETPDSQSPIIIDEFPPTLSSKTDSPSKLAREYTDLEVSHKSEI	945
886	QY	ANAPDGAAGSLPCTELPHDLISLKNIQKVEBKISFSDDFSKNGSATSKVLLLPDVSALGH	959
901	DB	ANAPDGAAGSLPCTELPHDLISLKNIQKVEBKISFSDDFSKNGSATSKVLLLPDVSALGH	1005
946	QY	TOAETESIVKPKVLKEAEKKLPDTEKEDRSPSAIFSDGLKTSVVDLLIYMRDIKKTGV	1019
960	DB	TOAETESIVKPKVLKEAEKKLPDTEKEDRSPSAIFSDGLKTSVVDLLIYMRDIKKTGV	1065
1006	QY	VFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAIQKSDGDEGHPFRAYLES	1079
1020	DB	VFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAIQKSDGDEGHPFRAYLES	1125
1066	QY	EVAISEELVQKYSNALSALGHVNCTIKELRRLFLVDLVDLSLKFAVLMMVFTVVGALFNGLT	1139
1080	DB	EVAISEELVQKYSNALSALGHVNCTIKELRRLFLVDLVDLVDLSLKFAVLMMVFTVVGALFNGLT	1178
1126	QY	LILALISLFSVPVTVYERHQAOIDHYLGLANKVNDAMAKIOAKIPGLKRAE	1192
1140	DB	LILALISLFSVPVTVYERHQAOIDHYLGLANKVNDAMAKIOAKIPGLKRAE	

RESULT 5  
US-09-893-348-23  
Sequence 23, application US/09893348  
Patent No. US20020072493A1  
GENERAL INFORMATION:  
APPLICANT: EISENBACH-SCHWARTZ, Michal  
APPLICANT: COHEN, Itzhak R.  
APPLICANT: BESERMAN, Pierre  
APPLICANT: MOSONEGO, Alon  
APPLICANT: MOALEM, Gila  
TITLE OF INVENTION: ACTIVATED T-CELLS, NE  
FILE REFERENCE: EIS-SCHWARTZ-2A  
CURRENT APPLICATION NUMBER: US/09/893,348  
CURRENT FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: US 09/314,161  
PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: US 09/218,277  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: PCT/US98/14715  
PRIOR FILING DATE: 1998-07-21  
PRIOR APPLICATION NUMBER: IL 124500  
PRIOR FILING DATE: 1998-05-19  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 23  
LENGTH: 1192  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-893-348-23

Query Match

Best Local Similarity 97.2%; Pred. No. 5.9e-261;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLDQSLVSSDSDPPRQPAFKYQFVREPEDEEEDEDEDEDELEVLKPKA 60  
Db MEDLDQSLVSSDSDPPRQPAFKYQFVREPEDEEEDEDEDEDELEVLKPKA 60

Qy 61 AGLSAAFPVTPAAGAPLMDGNDVFPAPRGPLPAAPVAPRQPSWDSPVSVSTVPAP 120  
Db 61 AGLSAAFPVTPAAGAPLMDGNDVFPAPRGPLPAAPVAPRQPSWDSPVSVSTVPAP 120

Qy 121 SPLSAAAVSPKLPEDDEPPAPPPPPASVSPQAEVPTVPAPAPAPPPSTPAAPKRG 180  
Db 121 SPLSAAAVSPKLPEDDEPPAPPPPPASVSPQAEVPTVPAPAPAPPPSTPAAPKRG 180

Qy 181 SSGA-----VVXXXXKIMDLKQPGNTISAGQEDFPVLETAASXPSLSP 226  
Db 181 SSGSVDETLPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPVLETAASXPSLSP 240

Qy 227 LSAAAPFKHEYLGNLSTVLPTGTLQENVSSEASKEVSEKATLLIDRLTTFESELEYSEM 286  
Db 241 LSAAAPFKHEYLGNLSTVLPTGTLQENVSSEASKEVSEKATLLIDRLTTFESELEYSEM 300

Qy 287 GSSFSVSPKASAVIVANPREEIIIVKNKDEEKLVSNNILHXQOELPTALTCLKVKEDEVV 346  
Db 301 GSSFSVSPKASAVIVANPREEIIIVKNKDEEKLVSNNILHXQOELPTALTCLKVKEDEVV 360

Qy 347 SSEKAKDSFNEKRVAVAPRREYADPKPFRVWEVKDSKEDSDMLAAGGKIESNLSKV 406  
Db 361 SSEKAKDSFNEKRVAVAPRREYADPKPFRVWEVKDSKEDSDMLAAGGKIESNLSKV 420

Qy 407 DKKCFADSLQTNHKEKSSNDTSPSTPEGIKDRSGAYITCAPNPAAATESIATNIF 466  
Db 421 DKKCFADSLQTNHKEKSSNDTSPSTPEGIKDRSGAYITCAPNPAAATESIATNIF 480

Qy 467 PLLDPTSENKTDKKEIKKAKQIVTEKNTSTKNSPFFVAAQDSETDYVTDNLTKVTE 526  
Db 481 PLLGDTSENKTDKKEIKKAKQIVTEKNTSTKNSPFFVAAQDSETDYVTDNLTKVTE 540

Qy 527 EVVANMPEGLTPDLVQACESELNEVGTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSP 586  
Db 541 EVVANMPEGLTPDLVQACESELNEVGTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSP 600

Qy 587 ESEATSPVLPDIIVMEAPLNSAVPSAGASVQPSGSPLEASSVNYESIKEHPENPPYE 646  
Db 601 ESEATSPVLPDIIVMEAPLNSAVPSAGASVQPSGSPLEASSVNYESIKEHPENPPYE 660

Qy 647 EAMSVSL-KVSGIKKEIKPENINAAQETAPYISACDLIKETKLSAPAPDPFSYSE 705  
Db 661 EAMSVSLKVGSGIKKEIKPENINAAQETAPYISACDLIKETKLSAPAPDPFSYSE 720

Qy 706 MAKVEQVPVHSELVSDSPDSEPVDFSDSIIPDVQKODETVMVKESLTETSPFSMI 765  
Db 721 MAKVEQVPVHSELVSDSPDSEPVDFSDSIIPDVQKODETVMVKESLTETSPFSMI 780

Qy 766 EYENKELSLAPPGGKPYLESFKLSLNDTKOTLLPDEVSTLSKKEKIPLOMBELSTAVY 825  
Db 781 EYENKELSLAPPGGKPYLESFKLSLNDTKOTLLPDEVSTLSKKEKIPLOMBELSTAVY 840

Qy 826 SNDDLPTSKAQIRETETPSDSSPIEIDEPPTLISKTDSFKLAREYTDLEVSHKSEI 885  
Db 841 SNDDLPTSKAQIRETETPSDSSPIEIDEPPTLISKTDSFKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAAGSLPCTELPHDLNLKNTQPKVBEKISFSDDPFKNGSATSKVLLLPDVSALGH 945  
Db 901 ANAPDGAAGSLPCTELPHDLNLKNTQPKVBEKISFSDDPFKNGSATSKVLLLPDVSALGH 959

Qy 946 TOAIESIVKPKVLEKAEKKLPDTEKEDRSPSAIFSAIDLGKTSVVDDLLYWRDIKKTGV 1005  
Db 960 TOAIESIVKPKVLEKAEKKLPDTEKEDRSPSAIFSAIDLGKTSVVDDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLLSLTVFSIVSTVYATALLSVTISFRIYKGVQIAQKSDGHPFRAYLES 1065  
Db 1020 VFGASLFLLLSLTVFSIVSTVYATALLSVTISFRIYKGVQIAQKSDGHPFRAYLES 1079

Db 1020 VFGASLFLLLSLTVFSIVSTVYATALLSVTISFRIYKGVQIAQKSDGHPFRAYLES 1079  
Qy 1066 EVAISEELVQKYSNSALGHVNCITIKELRRLFLVDLDVSLKFAVLMMVFTTVGALFNGLT 1125  
Db 1080 EVAISEELVQKYSNSALGHVNCITIKELRRLFLVDLDVSLKFAVLMMVFTTVGALFNGLT 1139  
Qy 1126 LLILALISLSPVPIYERHOAQIDHYHGLANVKNVDMAKIOAKIPGLKRAE 1178  
Db 1140 LLILALISLSPVPIYERHOAQIDHYHGLANVKNVDMAKIOAKIPGLKRAE 1192

RESULT 6  
US-10-267-502-429  
; Sequence 429, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 429  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-267-502-429

Query Match 98.1%; Score 5810; DB 15; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 5.9e-261;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLDQSLVSSDSDPPRQPAFKYQFVREPEDEEEDEDEDEDELEVLKPKA 60  
Db 1 MEDLDQSLVSSDSDPPRQPAFKYQFVREPEDEEEDEDEDEDELEVLKPKA 60

Qy 61 AGLSAAFPVTPAAGAPLMDGNDVFPAPRGPLPAAPVAPRQPSWDSPVSVSTVPAP 120  
Db 61 AGLSAAFPVTPAAGAPLMDGNDVFPAPRGPLPAAPVAPRQPSWDSPVSVSTVPAP 120

Qy 121 SPLSAAAVSPKLPEDDEPPAPPPPPASVSPQAEVPTVPAPAPAPPPSTPAAPKRG 180  
Db 121 SPLSAAAVSPKLPEDDEPPAPPPPPASVSPQAEVPTVPAPAPAPPPSTPAAPKRG 180

Qy 181 SSGA-----VVXXXXKIMDLKQPGNTISAGQEDFPVLETAASXPSLSP 226  
Db 181 SSGSVDETLPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPVLETAASXPSLSP 240

Qy 227 LSAAAPFKHEYLGNLSTVLPTGTLQENVSSEASKEVSEKATLLIDRLTTFESELEYSEM 286  
Db 241 LSAAAPFKHEYLGNLSTVLPTGTLQENVSSEASKEVSEKATLLIDRLTTFESELEYSEM 300

Qy 287 GSSFSVSPKASAVIVANPREEIIIVKNKDEEKLVSNNILHXQOELPTALTCLKVKEDEVV 346  
Db 301 GSSFSVSPKASAVIVANPREEIIIVKNKDEEKLVSNNILHXQOELPTALTCLKVKEDEVV 360

Qy 347 SSEKAKDSFNEKRVAVAPRREYADPKPFRVWEVKDSKEDSDMLAAGGKIESNLSKV 406  
Db 361 SSEKAKDSFNEKRVAVAPRREYADPKPFRVWEVKDSKEDSDMLAAGGKIESNLSKV 420

Qy 407 DKKCFADSLQTNHKEKSSNDTSPSTPEGIKDRSGAYITCAPNPAAATESIATNIF 466  
Db 421 DKKCFADSLQTNHKEKSSNDTSPSTPEGIKDRSGAYITCAPNPAAATESIATNIF 480

Qy 467 PLLDPTSENKTDKKEIKKAKQIVTEKNTSTKNSPFFVAAQDSETDYVTDNLTKVTE 526  
Db 481 PLLGDTSENKTDKKEIKKAKQIVTEKNTSTKNSPFFVAAQDSETDYVTDNLTKVTE 540

Qy 527 EVVANMPEGLTPDLVQACESELNEVGTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSP 586  
Db 541 EVVANMPEGLTPDLVQACESELNEVGTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSP 600

Qy 587 ESEATSPVLPDIIVMEAPLNSAVPSAGASVQPSGSPLEASSVNYESIKEHPENPPYE 646  
Db 601 ESEATSPVLPDIIVMEAPLNSAVPSAGASVQPSGSPLEASSVNYESIKEHPENPPYE 660

Qy 647 EAMSVSL-KVSGIKKEIKPENINAAQETAPYISACDLIKETKLSAPAPDPFSYSE 705  
Db 661 EAMSVSLKVGSGIKKEIKPENINAAQETAPYISACDLIKETKLSAPAPDPFSYSE 720

Qy 706 MAKVEQVPVHSELVSDSPDSEPVDFSDSIIPDVQKODETVMVKESLTETSPFSMI 765  
Db 721 MAKVEQVPVHSELVSDSPDSEPVDFSDSIIPDVQKODETVMVKESLTETSPFSMI 780

Qy 766 EYENKELSLAPPGGKPYLESFKLSLNDTKOTLLPDEVSTLSKKEKIPLOMBELSTAVY 825  
Db 781 EYENKELSLAPPGGKPYLESFKLSLNDTKOTLLPDEVSTLSKKEKIPLOMBELSTAVY 840

Qy 826 SNDDLPTSKAQIRETETPSDSSPIEIDEPPTLISKTDSFKLAREYTDLEVSHKSEI 885  
Db 841 SNDDLPTSKAQIRETETPSDSSPIEIDEPPTLISKTDSFKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAAGSLPCTELPHDLNLKNTQPKVBEKISFSDDPFKNGSATSKVLLLPDVSALGH 945  
Db 901 ANAPDGAAGSLPCTELPHDLNLKNTQPKVBEKISFSDDPFKNGSATSKVLLLPDVSALGH 959

Qy 946 TOAIESIVKPKVLEKAEKKLPDTEKEDRSPSAIFSAIDLGKTSVVDDLLYWRDIKKTGV 1005  
Db 960 TOAIESIVKPKVLEKAEKKLPDTEKEDRSPSAIFSAIDLGKTSVVDDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLLSLTVFSIVSTVYATALLSVTISFRIYKGVQIAQKSDGHPFRAYLES 1065  
Db 1020 VFGASLFLLLSLTVFSIVSTVYATALLSVTISFRIYKGVQIAQKSDGHPFRAYLES 1079

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 7.13706 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
Sequence: 1 SVDLLYWRDIKKTGVFGA.....VDMAKIQAKIPGLKRAE 189

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	927	99.6	199	2	US-08-700-607-1
2	927	99.6	201	4	US-09-949-016-9124
3	682	73.3	208	2	US-08-700-607-7
4	682	73.3	356	2	US-08-700-607-6
5	682	73.3	439	4	US-09-949-016-9180
6	682	73.3	776	2	US-08-700-607-5
7	682	73.3	776	4	US-09-949-016-6998
8	665	71.4	267	2	US-08-700-607-8
9	627.5	67.4	192	4	US-09-949-016-8859
10	541.5	58.2	168	4	US-09-149-476-563
11	518	55.6	219	4	US-09-270-767-45132
12	512	55.0	241	2	US-08-700-607-3
13	473.5	50.9	588	4	US-09-949-016-7290
14	285	30.6	92	4	US-09-149-476-411
15	246	26.4	114	4	US-09-513-999C-7861
16	144	15.5	374	4	US-09-248-796A-16008
17	100	10.7	80	3	US-08-905-223-411
18	89	9.6	468	4	US-08-487-596-8
19	89	9.6	468	4	US-08-660-451A-8
20	88.5	9.5	1278	4	US-09-462-136-2
21	88.5	9.5	1318	4	US-09-949-016-10152
22	88	9.5	382	4	US-09-949-016-11596
23	87.5	9.4	592	4	US-09-134-000C-5477
24	87.5	9.4	1051	3	US-09-134-001C-5005
25	85	9.1	414	4	US-08-956-171E-5246
26	85	9.1	414	4	US-08-781-986A-5246
27	83	8.9	744	4	US-09-785-381-1

28	83	8.9	744	4	US-09-785-381-3	Sequence 3, Appli
29	82.5	8.9	554	4	US-09-252-991A-27968	Sequence 27968, A
30	81.5	8.8	598	2	US-08-853-659A-53	Sequence 53, Appli
31	81	8.7	970	4	US-09-795-927-7	Sequence 7, Appli
32	80.5	8.6	280	4	US-09-543-681A-6175	Sequence 6175, Ap
33	80.5	8.6	593	4	US-09-328-352-4866	Sequence 4866, Ap
34	79.5	8.5	252	4	US-09-583-110-4880	Sequence 4880, Ap
35	79.5	8.5	257	4	US-09-107-433-4818	Sequence 4818, Ap
36	79	8.5	459	4	US-09-602-787A-302	Sequence 302, App
37	79	8.5	844	4	US-09-949-016-9438	Sequence 9438, Ap
38	79	8.5	993	4	US-08-836-687B-30	Sequence 30, Appli
39	78.5	8.4	446	4	US-09-543-681A-6579	Sequence 6579, Ap
40	78	8.4	292	4	US-09-489-039A-12212	Sequence 12212, A
41	78	8.4	349	4	US-09-198-452A-973	Sequence 973, App
42	78	8.4	358	4	US-09-438-185A-902	Sequence 902, App
43	77.5	8.3	383	4	US-09-248-796A-14833	Sequence 14833, A
44	77	8.3	154	1	US-08-366-783-5	Sequence 5, Appli
45	77	8.3	424	4	US-09-543-681A-7510	Sequence 7510, Ap

ALIGNMENTS

RESULT 1  
Sequence 1, Application US/08700607  
Patent No. 2858708

GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Auroving, Janice  
APPLICANT: Goli, Surya K.  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: Consensus  
US-08-700-607-1

Query Match 99.6%; Score 927; DB 2; Length 199;  
Best Local Similarity 100.0%; Pred. No. 7.9e-93;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VVDLLYWRDIKKTGVFGASLEFLLSLTVFVSIVVTAYIALALLSVTISFRIYKGVIOAI 61



Db 12 VDLYWRDIKKTGVVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAI 71  
Qy 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKPAVL 121  
Db 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKPAVL 131  
Qy 122 MVFTYVVGALFNGLTLLILALISLFSVPVYIERHQAQIDHYGLANKNVKDMAKIOAKI 181  
Db 132 MVFTYVVGALFNGLTLLILALISLFSVPVYIERHQAQIDHYGLANKNVKDMAKIOAKI 191  
Qy 182 PGLKKAEE 189  
Db 192 PGLKKAEE 199

## RESULT 2

US-09-949-016-9124  
; Sequence 9124, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIORITY FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9124  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9124

Query Match 99.6%; Score 927; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 8e-93;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDLYWRDIKKTGVVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAI 61  
Db 14 VDLYWRDIKKTGVVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAI 73  
Qy 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKPAVL 121  
Db 74 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKPAVL 133  
Qy 122 MVFTYVVGALFNGLTLLILALISLFSVPVYIERHQAQIDHYGLANKNVKDMAKIOAKI 181  
Db 134 MVFTYVVGALFNGLTLLILALISLFSVPVYIERHQAQIDHYGLANKNVKDMAKIOAKI 193  
Qy 182 PGLKKAEE 189  
Db 194 PGLKKAEE 201

## RESULT 3

US-08-700-607-7  
; Sequence 7, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 208 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307311  
US-08-700-607-7

Query Match 73.3%; Score 682; DB 2; Length 208;  
Best Local Similarity 68.4%; Pred. No. 3.8e-66;  
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

Qy 3 VDLYWRDIKKTGVVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAI 62  
Db 22 IDLYWRDIKKTGVVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAI 81  
Qy 63 KSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKPAVL 122  
Db 82 KSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKPAVL 141  
Qy 123 WVFTYVVGALFNGLTLLILALISLFSVPVYIERHQAQIDHYGLANKNVKDMAKIOAKI 182  
Db 142 WVFTYVVGALFNGLTLLILALISLFSVPVYIERHQAQIDHYGLANKNVKDMAKIOAKI 201  
Qy 183 GLKKAEE 189  
Db 202 GAKRHAEE 208

## RESULT 4

US-08-700-607-6  
; Sequence 6, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304